GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	cleic - nucleic search, using sw model	September 9, 2004, 13:30:05; Search time 23.9144 Seconds (without alignments) 3730.479 Million cell updates/sec	US-10-082-772B-1 21 1 ctgctttttatactaacttg 21	ng table: IDENTITY NUC Gapop 10.0, Gapext 1.0	hed: 3373863 seqs, 2124099041 residues	Total number of hits satisfying chosen parameters: 6747726	um DB seq length: 0 um DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	## See : N_Geneseq_29Jan04:* 1. geneseqn1980s:* 2. geneseqn1090s:* 3. geneseqn2000s:* 5. geneseqn2001bs:* 6. geneseqn2001bs:* 7. geneseqn2001bs:* 8. geneseqn2003bs:* 9. geneseqn2003bs:* 10. geneseqn2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ı	4000	Aaf5576 Recombina Aaf5576 PCR prime Aad14459 Recombina Acd28426 Wild type Acd28427 Engineere Acd2865 Wild tyne	19 m 0 m m 0 m 0 m 0 m
SUMMARIES	AAT37370 AAF61417 ABS76597 ACC44645	AAX78994 AAC55600 AAS06276 AAC87897 AAC87896	AAF55766 AAF55766 AAD14429 ACD28427 ACD28605	ACD28606 ADA38193 ADA38192 AAD60588 AAS06174 AAF61422 ABZ58727
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ALIGNMENTS

Site-specific recombination; bacterial attachment site; plasmid; vaccine; gene therapy; ss. A new expression cassette consists of a gene of interest controlled by a promoter and terminator functional in mammalian cells and is flanked by sequences in direct orientation which allow site-specific recombination. Lambda attp and attB sites specific recombination are the bacteriophage phage lambda. The expression cassettes can be used for producing plasmids which are useful in vaccination or for genetic/callular therapy, e.g. of amyotrophic lateral sclerosis; Alzheimer's or Parkinson's diseases, Plasmids capable of site-specific recombination - useful for vaccination and in gene therapy. coagulation/dyslipoproteinaemia or viral infections (AIDS or hepatitis) Wils P; Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other; Darquet A, Scherman D, Claim 17; Page 43; 81pp; French. Bacteriophage lambda attB site. (RHON) RHONE POULENC RORER SA. BP. 95FR-00002117. 96WO-FR000274. AAT37370 standard; DNA; 21 (first entry) Crouzet J, Bacteriophage lambda. WPI; 1996-402363/40. WO9626270-A1. 21-FEB-1996; 23-FEB-1995; 14-MAY-1997 29-AUG-1996. Cameron B, AAT37370; RESULT 1 AAT37370

Query Match

Matches

AAF61417;

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The invention describes producing a collection of responder cells for high throughput screening assays, by identifying and cloning regulatory regions into expression constructs to control nucleic acids, and introducing the constructs into addressable cells. The method is useful introducing the constructs into addressable cells. The method is useful in producing cells used in high throughput screening assays for profiling substances and conditions and for studying the function of the regulatory trepton mediating the response. The cells serve as biosensors to assess the effects of any perturbation, such as external or internal condition, on the cells from which the regulatory regions in the reporter gene constructs are derived can be inferred. This sequence represents a constructs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing a collection of responder cells for high throughput screening assays, comprises identifying and cloning regulatory regions into expression constructs to control nucleic acids, and introducing into
                                                           Responder cell; expression construct; screening assay; gene regulation;
blosensor; reporter gene construct; recombinase recognition site; ds.
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                                Recombinase recognition site attB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a muclaic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans anaimals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.
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                                                                                                                                                                                                                                                                                                                                                                        recombination; SSR; integrase; gene therapy; somatic;
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                                                                                                                                                                                                                                                                                                                                                                                                 targeted integration; attB; ds
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                                                                 Conservative
                                                                                                                                                                                                                                   AAF61417 standard; DNA;
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Best Local Similarity
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RESULT 2

AAF61417

DAF61417

AAF61417

AAF614

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Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
Nucleotide core region of attB SEQ ID NO:34.
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ABS76597;

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RESULT 3

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ABS76597

Matches

0

Gaps

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of chromosome. Also described: (I) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an Aces. (II) is useful for producing cransgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection, microphosometror of direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for an embryonic nucleic acid that encodes a therapeutic product which is useful for an embryonic nucleic acid that encodes a therapeutic product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
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                                                                                                                                                                                                                                                                       (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6; 272pp; English.
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21-MAR-2002; 2002US-0366891P.
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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector con an enclecules (VDMS) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific not recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMS, thereby producing one or more desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention
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                                                                               Fox DK;
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                                                                                                                                                                         Disclosure; Page 176; 185pp; English.
                                                                               Temple GF,
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                                                                                                                                         New nucleic acid cloning methods.
                                              (LIFE-) LIFE TECHNOLOGIES INC
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ID AAC55600 standard; DNA; 25 BP.
              98US-00177387.
 97US-0065930P
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24-OCT-1997;
              23-OCT-1998;
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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attB2, attL1, attL2, attB1, and attB2 nucleotide sequence. Also described are: (I) an isolated mucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites acond att recombination sites, and (2) an isolated mucleic acid molecule (III) comprising one or more mutated att recombination sites one mutated att recombination site and a second nucleic acid molecule comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising at second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated can recombinate to site and a second mucleic acid molecules. They can be used for changing vectors and methods from the present invention are used for the recombinational cloning of art recombination are used for the recombinational cloning of an uncleic acid molecules. They can be used for changing vectors, targeting desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (1), (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
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Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attL1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
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                                                                              Example 23; Page 157; 459pp; English
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09-MAR-2000; 2000US-0188020P.
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BRASCH M A.
TEMPLE G F.
HARTLEY J L.
BYRD D R N.
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(TEMP/)
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                                                                                                                                                                                                                                                                            AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrases (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising one or method of producing a population of hybrid acids comprising one or more recombination sites with at least one target nucleic acid comprising one or more recombination sites and causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins or peptides and they may also be used to express therapeutic proteins or peptides and they may also be used to each other. The method allows simultaneous cloning of two or more different nucleic acids
                                                   Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
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96US-00663002.
98US-00005476.
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WPI; 2001-356174/37.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Comprising a first nucleic acid sequence having a defined sequence (IAC87866 to AAC87881).

CAMC87866 to AAC87881, sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87861. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site; (2) an isolated nucleic acid molecule (III) comprising a first at recombination site or avoids hairpin for mutated molecule (III) and to rose second molecule (III) comprising a first att recombination site comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining consineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. The present sequence represents an E. coli atts oligonuclectide, which is used in an example from the present invention The present invention describes an isolated nucleic acid molecule (I) %XGGGGGGGGGGGGGGGGGG

Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

100.0%; Score 21; DB 4; Length 25; 0; Indels Pred. No. 23; Mismatches 1 CIGCTITITIATACTAG 21 N .; 22 CTGCTTTTTATACTACTTG 100.08; Local Similarity 100. 1es 21; Conservative Query Match Best Loca Matches ď g

AAC87896 standard; DNA; 25 02-MAR-2001 AAC87896; RESULT 9 AAC87896

(first entry)

Escherichia coli attB oligonucleotide SEQ ID NO:31.

Core region, recombination site; cloning; chimeric DNA; PCR primer; characteristic; mutation; att site; lox site; phoA gene; ss.

Escherichia coli.

JS6143557-A.

07-NOV-2000.

99US-00233493. 20-JAN-1999;

Hartley JL, Brasch MA; WPI; 2001-136877/14.

> 95US-00486139. 98US-00005476. 96US-00663002 07-JUN-1995; 12-JAN-1998; 07-JUN-1996

(LIFE-) LIFE TECHNOLOGIES INC.

Brasch MA, Hartley JL;

WPI; 2001-049004/06.

Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered mutation.

Example 3; Col 24; 73pp; English.

The present invention describes an isolated nucleic acid molecule (1) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881, sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first

ó recombination site or avoids hairpin formation, the recombination site or avoids hairpin formation, the recombination site or avoids hairpin formation, the recombination site comprising a direct att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids, and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a corregion of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining nearest encombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. The present sequence represents an E. coli attB oligonucleotide, which is mutated recombination site that removes one or more stop codons from the Gaps 0; 100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23; 0; Indels Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other; used in an example from the present invention Mismatches Recombination site; cloning; att; ss. 1 CTGCTTTTTTATACTAACTTG 21 24 0; 4 CTGCTTTTTATACTAACTTG (LIFE-) LIFE TECHNOLOGIES INC. AAF55765 standard; DNA; 25 BP. 95US-00486139. 96US-00663002. 98US-00005476. 12-APR-2001 (first entry) Recombination site attBwt. 21; Conservative Best Local Similarity 12-JAN-1998; 07-JUN-1995; Unidentified US6171861-B1 09-JAN-2001. AAF55765; Matches RESULT 10 **AAF**55765 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ à g

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Gaps

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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chiercir nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host. Example 3; Col 23; 73pp; English. invention us-10-082-772b-1.rng

Matches

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g

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The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/ partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing vectors, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., PCR products (with an attB site at one end and a loxe site at the other end), genomic DNAs, and cDNAs. The methods are highly specific, rapid, and less labour intensive than prior art methods. The present sequence is a recombination site useful for recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for apposing nucleic acids comprising an expression signal and a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination.
                                                                                                                           site; copy number; replicon; recombinatorial cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild type attL and attR site recombination sequence attB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector donor DNA; ds; flanking recombination site; attB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                  Recombination site attBwt wild type DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCTTTTTTATACTAGCTTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Col 23; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                    95US-00486139.
96US-00663002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACD28426 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488248/53.
                                                                                                                           Recombination
                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                 US6270969-B1
                                                                                                                                                                                                                                                                                                               20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                         01-NOV-2001
                                                                                                                                                                                                                                                                        07-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartley JL,
                                                                                                                                                   attBwt; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
    AAD14459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACD28426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a PCR primer used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host.
                                                                                      Gaps
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                                         Length 25;
                                                                                  0; Indels
Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                    100.0%; Score 21; DB 4;
100.0%; Pred. No. 23;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombination site; cloning; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 43-44; 73pp; English
                                                                                                                           1 CTGCTTTTTTATACTAGCTTG 21
                                                                                                                                                   CTGCTTTTTATACTAACTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTTTTTTATACTAACTTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIFE-) LIFE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                      AAF55766 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-136877/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             PCR primer #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6171861-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1996;
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                                                                                                                                                                                                                                                                                                             AAF55766;
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                                         Query Match
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0,

Gaps

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0; Indels

Matches

RESULT 12 AAD14459 ID AAD1 XX

Dp

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Making Cointegrate DNA molecule, by combining recombination sites flanking the desired DNA segment in insert donor DNA, with the recombination sites of vector donor DNA, using site specific
              HART/) HARTLEY J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-540884/51.
                                                                WPI; 2003-540791/51
                        (BRAS/) BRASCH M A.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   associated DNA #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003068799-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           22
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                                                                                                                      marker.
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                The invention relates to a vector donor DNA molecule comprising a first DNA segment and a second DNA segment containing at least one selectable marker. The first and second segments are separated either by, in a circular vector donor, a first and a second recombination site, or in a linear vector donor, at least a first recombination site, where each pair of flanking recombination sites are engineered and do not recombine with each other. The nucleic acid molecule, vectors and methods are useful for moving or exchanging segments of DNA molecules using engineered recombination sites and recombination proteins to provide chimeric DNA molecules that have the desired characteristic(s) and/or DNA segment(s).
                                                                                                                                                                                        New Vector Donor DNA molecule for recombinational cloning using engineered recombination sites, comprises first and second DNA segments that do not recombine with each other and that contain a Selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the wild type attL and attR site recombination sequence attB
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; ds; flanking recombination site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engineered recombination site associated DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 8
Pred. No. 23;
; Mismatches
                                                                                                                                                                                                                                                Example 3; Page 13; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CIGCTITITIATACIAACITG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 crecirririaracraacrie
                                                            95US-00486139.
96US-00663002.
99US-00233493.
99US-00432085.
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ACD28427 standard; DNA; 25 BP
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96US-00663002.
99US-00233493.
99US-00432085.
                                         2002US-00058291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-00058291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                 Brasch MA;
                                                                                                                HART/) HARTLEY J L.
                                                                                                                                                                      WPI; 2003-540791/51
                                                                                                                            BRASCH M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
US2003064515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003064515-Al.
                                        30-JAN-2002;
                                                                                 20-JAN-1999;
02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector donor
                                                            07-JUN-1995;
                                                                        07-JUN-1996;
                                                                                                                                                 Hartley JL,
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20-JAN-1999;
02-NOV-1999;
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                    03-APR-2003
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                                                                                                                             BRAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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The invention relates to a vector donor DNA molecule comprising a first DNA segment and a second DNA segment containing at least one selectable marker. The first and second segments are separated either by, in a circular vector donor, a first and a second recombination site, or in a linear vector donor, at least a first recombination site, where each pair of flanking recombinatic sites are engineered and do not recombine each other. The nucleic acid molecule, vectors and methods are useful for moving or exchanging segments of DNA molecules using engineered
                                                                                                                                                                                  sedments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombination sites and recombination proteins to provide chimeric DNA molecules that have the desired characteristic(s) and/or DNA segment(s) The present sequence represents the engineered recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                           New Vector Donor DNA molecule for recombinational cloning using engineered recombination sites, comprises first and second DNA segmethat do not recombine with each other and that contain a Selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 8; Length 25;
Pred. No. 23;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cointegrate DNA; flanking recombination site; ds; attBwt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             Disclosure; Page 24; 71pp; English.
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96US-00663002.
99US-00233493.
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Hartley JL, Brasch MA;
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Example 3; Page 14; 71pp; English.

XX
The invention relates to a method of making a cointegrate DNA molecule.
CC The method is useful for making a cointegrate DNA molecule. The method is useful for a variety of DNA exchanges, such as subcloning of DNA, in
CC the CDNA segments using recombination proteins. The method is highly
CC vitro or in vivo. The method enables efficient and specific recombination
CC view of DNA segments using recombination proteins. The method is highly
CC yield and speed of the method facilitates DNA or RNA subcloning,
CC yield and speed of the method facilitates DNA or RNA subcloning,
CC yield and schange useful for other related purposes. Since single
CC molecules of the recombinations product can be introduced into a
CC biological host, propagation of the desired product DNA in the absence of
CC other DNA molecules is more readily realised. Reaction conditions can be
CC sequence represents the wild type attl and attr site recombination
XX
Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
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Ouery Match 100.0%; Score 21; DB 8; Length 25; Best Local Similarity 100.0%; Pred. No. 23; Matches 21; Conservative 0; Mismatches 0; Indels Qy | CIGCTTTTTATACTAACTTG 21

Db 4 CIGCTTTTTTATACTAACTTG 24

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0; Gaps

Search completed: September 9, 2004, 18:05:38
Job time : 25.9144 secs

us-10-082-772b-1.rnpb

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Sequence 13, Appl
Sequence 95, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
                                                                                                              9, 2004, 19:34:38; Search time 26.5292 Seconds (without alignments) 3982.858 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 34, A
Sequence 45, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: cgn2 6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: cgn2 6/ptodata/2/pubpna/US07_NEW PUB.seq:*
3: cgn2 6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: cgn2 6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: cgn2 6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6: cgn2 6/ptodata/2/pubpna/US08_NEW PUB.seq:*
7: cgn2 6/ptodata/2/pubpna/US08_NEW PUB.seq:*
8: cgn2 6/ptodata/2/pubpna/US08_DEW PUB.seq:*
10: cgn2 6/ptodata/2/pubpna/US08_DEW PUB.seq:*
11: cgn2 6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: cgn2 6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: cgn2 6/ptodata/2/pubpna/US09_NEW PUB.seq:*
13: cgn2 6/ptodata/2/pubpna/US09_NEW PUB.seq:*
14: cgn2 6/ptodata/2/pubpna/US09_NEW PUB.seq:*
15: cgn2 6/ptodata/2/pubpna/US09_NEW PUB.seq:*
16: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
17: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
18: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
19: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
19: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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19: cgn2 6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-252-384-6
US-10-161-403-445
US-10-097-034A-45
US-09-732-914-95
US-09-97-2914-95
US-09-907-200-60
US-09-907-000-60
US-09-907-000-60
US-09-907-000-60
US-09-432-085-31
US-09-432-085-31
US-09-432-085-32
US-09-85-488-60
US-10-680-316-60
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                                                                                                                                                                                                                                                                                                                                3304383 seqs, 2515761380 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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21
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Match 1
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Perfect score:
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ALIGNMENTS

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APPLICANT: Beatrice CAMERON
APPLICANT: Pierre WILS
APPLICANT: Pierre WILS
APPLICANT: Anne-Marie DARQUET
TITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
FILE REFERENCE: MINICIRCLE
CURRENT APPLICATION NUMBER: US/09/981,803
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATEUTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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        Sequence 3, Application US/09981803
Publication No. US20030032092A1
GENERAL INFORMATION:
APPLICANT: Joel CROUZET
APPLICANT: Daniel SCHERMAN
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ORGANISM: Artificial sequence
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Best Local Similarity
US-09-981-803-3
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
LENGTH: 21
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RESULT 2 US-10-252-384-6 ; Sequence 6, Application US/10252384

21

CTGCTTTTTATACTAACTTG

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US-10-097-034A-45

Sequence 45, Application US/10097034A

Publication No. US20040076954A1

GENERAL INFORMATION:
APPLICANT: Bu, Andrew
APPLICANT: Caldwell, John
APPLICANT: Caldwell, John
APPLICANT: Caldwell, John
APPLICANT: Caldwell, John
ASSAYS, Development Thereof,
TITLE OF INVENTION: Collections of Cellular Reporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-310-695-13

Sequence 13, Application US/10310695

Publication No. US20040110293A1

GENERAL INFORMATION:

APPLICANT: BNGGE, BETER

APPLICANT: ENENEL, BARBARA

TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS

TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
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Pred. No. 18:
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Pred. No. 18;
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILLE REFERENCE: 38417-1311
CURRENT APPLICATION NUMBER: US/10/097,034A
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,148
PRIOR APPLICATION NUMBER: 60/275,148
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
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           CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR PRILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
PRIOR PILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FRACESQ for Windows Version 4.0
SEQ ID NO 34
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                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 21; Conservative
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; OTHER INFORMATION: attB
US-10-161-403-34
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Best Local Similarity
Matches 21; Conserv
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                                                                                               WILS, Pierre
DARQUET, Anne-Marie
TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
USE THEREOF IN GENE THERAPY
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COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/252,384

FILING DATE: 24-Sep-2002

CLASSIFCATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/894,511

APPLICATION NUMBER: US/08/894,511
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100.0%; Pred. No. 18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Savitary Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
TELECOMMUICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: «Unknown»
APPLICATION NUMBER: FR 95/02117
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CIGCITITITATACTAACTIG 21
                                                                   SCHERMAN, Daniel
CAMERON, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perez, Carl
Lindenbaum, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
  Publication No. US2003010444A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELBFAX: (610) 454-
INFORMATION FOR SEQ ID NO: 6:
                     GENERAL INFORMATION:
APPLICANT: CROUZET, JOEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Greene, Amy
Leung, Josephine
Fleming, Elena
Stewart, Sandra
Shellard, Joan
                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-161-403-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-252-384-6
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gard.
APPLICANT: Temple, Gard.
APPLICANT: Temple, Gard.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,900
CURRENT APPLICATION NUMBER: 09/177,387
PRIOR PILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
IENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60, Application US/09907719
Publication No. US20020192819A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Frombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE REFERENCE: 0942.2850004
CURRENT APPLICATION UMBER: US/09/907,719
CURRENT FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
                                                                                                                                                                                       OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 21; DB 9; Length 25; Best Local Similarity 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/09907900 Patent No. US20020172997A1
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PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                             ORGANISM: Unknown
                                                                                                                                                                                                                                           US-09-855-797A-60
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US-09-907-719-60
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                                                                                                                           TYPE: DNA
                                                                                                                                                                           FEATURE:
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Sequence 95, Application US/09732914

Patent No. US20020007051A1

SEGNERAL INFORMATION:

APPLICANT: Cheo, David

APPLICANT: Ensek, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Byrd, Devon R.N.

TITLE OF INVENTION: Recombinational Cloning

FILE REFERENCE: 0942.501002

FILE REFERENCE: 0942.501002

FILE REPERENCE: US 60/169,983

PRIOR APPLICATION NUMBER: US 60/169,983

PRIOR FILING DATE: 2000-12-11

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patentin version 3.0

SEQ ID NO 95

LEGGTH: 25

LEGGTH: 25
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Fatent No. US20020094574A1

GENERAL INFORMATION

APPLICANT: Hartley, James L.

APPLICANT: Femple, Gary F.

APPLICANT: Femple, Gary F.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION NUMBER: US/09/855,797A

CURRENT APPLICATION NUMBER: 09/296,281

FRIOR PRIOR PILING DATE: 1999-04-22

PRIOR APPLICATION NUMBER: US 60/065,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                      Length 21;
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                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 17; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                     Mismatches
  FILE REFERENCE: DEBE:019US
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                  1 CTGCTTTTTTATACTAACTTG 21
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
                                                                                                                                                                        TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: attB0
US-09-732-914-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-855-797A-60
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Gaps

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US-09-432-02/c
; Sequence 32, Application US/09432085
; Publication No. US2030100110A1
; Publication No. US2030100110A1
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                     Length 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER: ELORDY disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: PARENTEN: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
TITING DATE: (Herewith)
                                     Score 21; DB 10;
Pred. No. 19;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 10; 100.0%; Pred. No. 19;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION:
TELECHOMICICATION:
TELECHOMICICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION BATA:
PRIOR APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
            100.0%; Scu
100.0%; Pre
0;
                                                                                                                                                           21
                                                                                                                                                                                                                   4 CIGCILITITATACIAACTIG 24
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                                                                                             21; Conservative
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Best Local Similarity 100.(
Matches 21, Conservative
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STRANDEDNESS: both
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MOLECULE TYPE: CDNA
US-09-432-085-32
                                     Query Match
Best Local Similarity
                                                                                                Matches
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                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-907-719-60
                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09432085
Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 09/63,002
FILING DATE: 09-JUN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 09-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 09-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 9; 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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CMPUTER READABLE FORM:
CMPUTER: FLORDS disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/486,13
FILING DATE: 07-UNN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
1.RNGTH: 25 base pairs
NUMBER OF SEQ ID NOS: 60
SOFTWARRE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 21, Conservative
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STRANDEDNESS: both
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                                                                                                                      TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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; MOLECULE TYPE:
US-09-432-085-31
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US-09-432-085-31
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TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
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Publication No. US20030064515A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 13; Length 25; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,291
FILING DATE: 30-Jan-2002
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              Sequence 31, Application US/10058291
Publication No. US20030064515A1
GENERAL INFORMATION:
                 4 CIGCITITITATACTAACTIG 24
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                                                                                                                                                                                              APPLICANT: Hartley, James L. Brasch, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
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CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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Best Local Similarity
Matches 21; Conserv
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                                                                                RESULT 14
US-10-058-291-31
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US-09-985-448-60

US-09-985-448-60

Sequence 60, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.285004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 60

LENGTH: 25

LENGTH: 25
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Publication No. US20040063207A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942-2860004

CURRENT FLING DATE: 2003-10-08

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-24

NUMBER OF SEQ ID NOS: 60
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US-10-680-316-60
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SEQ ID NO 60
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-985-448-60
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
COUNTY: USA
ZIP: 2000-3934

COUNTY: USA
ZIP: 2000-3934

COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Lam PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,291
FILING DATE: 30-432,085
FILING DATE: 139-11-02
APPLICATION NUMBER: 09/432,085
FILING DATE: 12-JAN-1999
APPLICATION NUMBER: 09/663,002
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION STREEPRAYION:
TELEPRAX: 202-371-2600
INPORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERICYTES:
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100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: CBNA

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-058-291-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Search completed: September 10, 2004, 00:14:06 Job time : 27.5292 secs

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September 9, 2004, 15:48:15; Search time 144.957 Seconds (without alignments) 6279:120 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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em_htgo_other:*
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Maximum DB seq length: 2000000000
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1: gb ba:*
3: gb hrg:*
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em_on: *
em_or: *
em_ov: *
em_pot: *
em_pl: *
em_ro: *
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	AR265736 Sequence AX092112 Sequence	ARIZ4551 Sequence ARIZ4552 Sequence	AR163202 Sequence	AR163203 Sequence	AX491670 Sequence	AX498641 Sequence	BD131386 Recombina AR142201 Sequence	AR142202 Sequence	A46167 Sequence 5	Afolds Sequence S AR361092 Sequence	AR361093 Sequence	AA/8/502 Sequence AR265731 Sequence	AR265732 Sequence	AR265752 Sequence	AR142203 Sequence	AR265753 Sequence	J01638 E.coli ATT	U39938 Escherichia	AR131048 Sequence RD235468 Control o	Sequence	AR350177 Sequence	BD235469 Control o	AR261941 Sequence	AKSSU1/8 Sequence A38246 Sequence 1	A38251 Sequence 6	A93674 Seguence 1 A93679 Seguence 6	AR101809 Seguence	0,0	57 Escher	4.	AX/8/505 Sequence BD263306 Compositi		linear PAT 10-APR-2003			ils,P. and Darquet,AM. gene transfer
SUMMARIES	AR265736 AX092112	AK124551 AR124552	AR163202	AR163203	AX491670	AX498641	BD131386 AR142201	AR142202	A46167	A46168 AR361092	AR361093	AX /8 / 502 AR265731	AR265732	AR265752	AR142203	AR265753	ECOLAMATT	ECU39938	AR131048 RD335468	AR261940	AR350177	BD235469	AR261941	AK3501/8 A38246	A38251	A93674 A93679	AR101809	AR101810		750	8750 6330	ALIGNMENTS	t-	US 6492164.		., Cameron,B., W n cassettes for 10-DEC-2002; ifiers
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Result No. Scor	1 7 8 8		ינה		~ œ				13				170	200										ى د 1. ك	36		3 6 6	0 4 0		57	H H		RESULT 1 AR265736	DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES

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PAT 16-MAY-2001
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Harrley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861-A 32 09-JAN-2001;
Location/Qualifiers
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1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
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Hartley, J.L. and Brasch, M.A.
Recombinational cloning using enginer
Patent: US 6270969-A 31 07-AUG-2001;
Location/Qualifiers
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Sequence 32 from patent US 6171861.
AR124552
AR124552.1 GI:14109913
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Sequence 31 from patent US 6270969.
AR165202 4R163302.1 GI:16233722
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Sequence 32 from patent US 6270969.
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Enterobacteriaceae; Escherichia.
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Unclassified.
1 (bases i to 25)
1 (bases i to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: WS 6171864-A 31 09-JAN-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
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21; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0;
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Sequence 31 from patent US 6171861.
AR124551
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AX092112
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AX092112
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AR124551
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Sequence 31 from Patent BP1229113.
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JP 2002500861-A/60.
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AX498641
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PN JP 2002537790-A/91
PD 12-NCV-2002
PF 02-MAR-2000 UP 2000602252
PF 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC C12N15/09; COFK14/00,C12N1/15,C12N1/19,C12N1/21,C12N15/10,C12N15/PC
                                                                                                                                                                                                                                                                                                                                                                                  artificial sequences.

1 (bases 1 to 25)

Hartley,J.L. Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
nucleic acids
Patent: JP 2002537790-A 91 12-NOV-2002;
INVITROGEN CORP
                                                                                                                                                                                                                                                       Compositions and methods for use in recombinational cloning of nucleic acids.
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Patent: US 6270969-A 32 07-AUG-2001;
Location/Qualifiers
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Sequence 31 from Patent EP1227147.
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BD111386 25 bp DNA linear PAT 18-SEP-2002
Recombinational cloning using nucleic acids having recombination
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1 (bases 1 to 25)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Recombinational cloning using nucleic acids having recombination
Patent: JP 2002500861-A 60 15-JAN-2002,
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PD 15-JAN-2002
PF 26-OCT-1999 JP 200518069
PR 24-OCT-1997 US 60/065330,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
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Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 31 07-AUG-2002;
INVITROGEN CORPORATION (US)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: FP 1227147-A 31 31-JUL-2002;
INVITROGEN CORPORATION (US)
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/db xref="taxon:32644"
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FEATURES

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PAT 07-MAR-1997
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METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
PATENT: WO 9521914-A 5 17-AUG-1995;
PASTED MERIBUX SERUMS VACC (FR)
Other Publication AU 1666895 950829
Other publication FR 2715940 950811.
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METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
BARRESSION VECTORS
Patent: WO 9521914-A 6 17-AUG-1995;
PASTEDW MERIEUX SERUMS VACC (FR)
OCHER Publication AU 1666895 950829
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Sequence 5 from Patent WO9521914.
A46167
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A46168.1 GI:2300416
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C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
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Sodoyer,R., Aujame,L., Geoffroy,F. and Bouchardon,A.
Preparation of a multicombinatorial library of antibody gene
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Sodoyer,R., Aujame,L., Geoffroy,F. and Bouchardon,A.
Preparation of a multicombinatorial library of antibody gene
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Patent: US 6174708-A 7 16-JAN-2001;
Location/Qualifiers
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Patent: US 6174708-A 8 16-JAN-2001;
Location/Qualifiers
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ARI42201.
ARI42201.1 GI:15102501
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Sequence 8 from patent US 6174708.
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REFERENCE AUTHORS TITLE

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RESULT 12 AR142202/c LOCUS

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Unknown.

(ISM Unknown.

Unclassified.

NCE 1 (bases 1 to 27)

(ORS Sodoyer,R., Aujame,L. and Geoffroy,F.

LE Process for preparing a multicombinatorial library of vectors for expressing antibody genes

JRNAL Patent: US 6595697-A 5 29-UU.-2003;

URBS Location/Qualifiers

Location/Qualifiers

1. 27

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                                   PAT 17-AUG-2003
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Sequence 5 from patent US 6599697.
AR361092 AR361092.1 GI:33768795
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'GgDZ_6/ptodata2/ina/5A_COMB.seq:*
'GgDZ_6/ptodata2/ina/5B_COMB.seq:*
'GgDZ_6/ptodata2/ina/6A_COMB.seq:*
'GgDZ_6/ptodata2/ina/6A_COMB.seq:*
'GgDZ_6/ptodata2/ina/6B_COMB.seq:*
'GgDZ_6/ptodata2/ina/eB_COMB.seq:*
'GgDZ_6/ptodata2/ina/backfilesI.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-101-629A-7
US-09-101-629A-8
US-08-693-234-5
US-08-693-234-6
US-08-894-511-1
US-09-655-728-1
US-09-655-728-2
US-09-655-728-2
US-08-894-511-2
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US-09-101-629A-9
US-08-894-511-23
US-09-655-728-23
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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21
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Match Length
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Perfect :
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ALIGNMENTS

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Sequence 31, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TILLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                              ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/23,493
FILING DATE: 20-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/66139
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
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FILING DATE: 07-JUN-1995
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TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                       USA
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STATE: D
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND USE THEREOF IN GENE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IDAPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/655,728
FILING DATE: 05-Sep-2000
CLASSIFICATION BARA:
PRING DATE: 40known>
PROPLICATION DATE: 40known>
PROPLICATION NUMBER: 08/894,511
FILING DATE: 40known>
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                            Score 21; DB 3; Length 21; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21; DB 4; Length 21;
Pred. No. 1.5;
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ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ST95013-US
                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                                              SCHERMAN, Daniel
CAMERON, Beatrice
WILS, Pierre
DARQUET, Anne-Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
                                                                                                                              1 CTGCTTTTTATACTAACTTG 21
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1 Similarity 100.0%;
21; Conservative 0;
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STRANDEDNESS: double
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                                          Query Match
Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 21; Conserv
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US-09-655-728-6
US-08-894-511-6
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Version #1.30

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Fatent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered;
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
100.0%; Score 21; DB 3; Length 25; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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Sequence 32 Application US/0905476

Sequence 32 Application US/09055476

Patent No. 617180

APPLICANT: Hartley, James L.
APPLICANT: Harsch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: MS/09/005,476
FILING DATE: herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                    CIGCITITITATACIAACTIG 24
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TELECOMMUNICATION INFORMATION:
TELERAN: 202-371-260
TELERAX: 202-371-260
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
TOPOLOGY: both
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Sequence 31, Application US/09005476
| Patent No. 6171861
| GENERAL INFORMATION:
| APPLICANT: Hartley, James L.
| APPLICANT: Brasch, Michael A.
| TITLE OF INVENTION: Recombinational Cloning Using Engineered
| TITLE OF INVENTION: Recombination Sites
| STREET: 1100 New York Ave., N. W. Suite 600
| CITY: Washington STATE: DC
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE ISPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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herewith
1.
                                                                                                                                                                                                            CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRICR APPLICATION BATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRICR APPLICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
CLASSIFICATION:
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APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 base pairs
                    ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: CDNA
US-09-233-493-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          both
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US-09-005-476-31
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Gaps

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GREERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2865007

CURRENT APPLICATION NUMBER: US 09/177,387

BARLIER FILING DATE: 1998-10-23

BARLIER FILING DATE: 1998-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                     PILING DATE: 20-JAN-1999
CLASSIFICATION: 20-JAN-1999
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: BLING DATE: 07-JUN-1996
CLASSIFICATION TOWBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION TOWBER: 08/486,139
FILING DATE: 07-JUN-1995
ITELEPHONE: 202-371-2600
ITELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCTTTTTATACTAACTTG 21
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
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Best Local Similarity 100.(
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: bot
; MOLECULE TYPE:
US-09-233-492-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-296-280-60
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LENGTH: 25
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APPLICANT: Barsch, Michael A.
IITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
STREET: Machington
STREET: About 100 New York Ave., N. W. Suite 600
STREET: Machington
                                                                                        APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3-
CORRESPONDENCE ADDRESS:
ADDRESSER: GERENE, GER
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US-09-233-492-32/c
US-09-233-492-33-492
; Sequence 32, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
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ZIP: 20005-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 31, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCTTTTTATACTAACTTG 21
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATH:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                  FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
                                     ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCTTTTTTATACTACTTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
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TOPOLOGY: both
MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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Fatent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES. 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
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                                                                                                  APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SECUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 4; Length 25; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 31, Application US/09498074 Patent No. 6534264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
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TELEFAN: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                        Washington
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          20005-3934
                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       USA
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US-09-498-074-32/C
                       US-09-498-074-31
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RESULT 10
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0;

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Search completed: September
Job time : 5.63035 secs
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                                                                                                              SEQ ID NO 8
LENGTH: 26
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APPLICANT: Sodoyer, Regis
APPLICANT: Sodoyer, Regis
APPLICANT: Bouchardon, Annabelle
APPLICANT: Bouchardon, Annabelle
APPLICANT: Bouchardon, Annabelle
TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
TITLE OF INVENTION: Gene Expression Vectors
TITLE OF INVENTION: 1999.201-12
CURRENT APPLICATION NUMBER: US/09/101,629A
CURRENT APPLICATION NUMBER: PCT/FR96/01938
FRIOR FILING DATE: 1996-12-04
NUMBER OF SEQ ID NOS: 36
SEQ ID NOS: 36
SEQ ID NO 7
LENGTH: 26
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APPLICANT: Geoffroy, Frederique
APPLICANT: Bouchardon, Annabelle
TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
TITLE OF INVENTION: Gene Expression Vectors
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                                                                                                                                                                                                                                 DB 5; Length 25;
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CURRENT APPLICATION NUMBER: US/09/101,629A
CURRENT FILING DATE: 1999-01-12
                                                                                                                                                                                                                                   Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                           1 CTGCTTTTTTATACTAGCTTG 21
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Patent No. 6174708
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                TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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1 Similarity 100.0%; P:
21; Conservative 0;
TELECOMMUNICATION INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Sodoyer,
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US-09-101-629A-8/c
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GENERAL INFORMATION:
APPLICANT: SODOYER, ET AL
TITLE OF INVENTION: PROCESS FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF VECTORS FOR
TITLE OF INVENTION: EXPRESSING ANTIBODY GENES
FILE REFERENCE: P03144USO/BAS
CURRENT APPLICATION NUMBER: US/08/693,234
CURRENT PILING DATE: 1996-00-04
PRIOR PILING DATE: 1995-02-02
PRIOR FILING DATE: 1995-02-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PALCHIN VERSION 3.1
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Pred. No.
PRIOR APPLICATION NUMBER: PCT/FR96/019:
PRIOR FILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: FR 95 14 325
PRIOR FILING DATE: 1995-12-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
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US-08-693-234-5
; Sequence 5, Application US/08693234
; Patent No. 6599697
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Best Local Similarity 100.0%;
                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 21; Conservative
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9, 2004, 21:21:16

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Run

Sequence:

Searched:

Database

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AQ990174 REC00899
AQ991338 REC0255
AQ99138 REC0255
AQ991058 REC0129
AQ990513 REC01299
AQ990513 REC01299
AQ990513 REC01299
AQ990101 REC01864
AQ991211 REC01894
AQ991211 REC01894
AQ991211 REC01894
AQ991315 REC0132
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AQ991315 REC01208
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AQ99031 REC01106
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AQ99031 REC0126
AQ99031 REC02368
AQ991791 REC0239
AQ991791 REC02368
AQ991791 REC0239
AQ991791 REC
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Photorhabdus luminescens
Photorhabdus luminescens
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaces; Photorhabdus.
1 (Dases 1 to 427)
Ifrach-Constant, F.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                             BX460736 BX460736
BX362060 BX362060
AL549604 AL549604
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Rfc00900 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00900, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
             AQ991338
AQ981578
AQ991068
AQ990513
AQ990758
AQ991011
                                                                                                          AQ991241
AQ991039
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AQ990809
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AQ980861
AQ990110
AQ990301
AQ990470
AQ990388
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AQ991791
CC546560
BX329593
BX341052
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BX419333
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BX459157
BX441486
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BX362060
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AQ991352
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  sequence.
AQ990175
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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MEDLINE
PUBMED
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AQ990175
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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AQ990483 R£C01260
AQ990485 R£C01263
AQ990287 R£C01035
                                                                               9, 2004, 17:30:16; Search time 169.634 Seconds (without alignments) 3696.811 Million cell updates/sec
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                                                                                                                                                                                                                                        55026578
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                 27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                           sw model
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AQ990483
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Maximum Match 100%
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length: 2000000000
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Match Length
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Maximum DB seq
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Perfect score:
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GSS 14-AUG-2000

21 21 21 21 21

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No.

Result

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Gaps

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GSS 14-AUG-2000

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1 (bases 1 to 469)
Liferach-Constant, F.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                  /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                    AQ990485
Rfc01263 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01263, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                         Length 450;
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/mol_type="genomic DNA"
/strain="W14"
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100.0%; Pred. No. 5.5e+02;
iive 0; Mismatches 0;
                                                                                                         Score 21; DB 28;
Pred. No. 5.6e+02;
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Department of Biology and Biochemistry
University of Bath
                                                                                                                                                     Mismatches
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG01263"
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AQ990485.1 GI:9649079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Famil: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to B.
                    This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae, Photorhabdus.
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Rfc01260 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01260, genomic survey
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/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                 'organism="Photorhabdus luminescens"
mol_type="genomic DNA"
strain="W14"
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/clone="PLG00900"
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Class: shotgun.
Location/Qualifiers
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  Email: bssrfc@bath.ac.uk
                                                                                                            Seq primer: M13 Forward
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AQ990483.1 GI:9649077
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Rfc00899 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00899, genomic survey
  GSS 14-AUG-2000
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1 (bases 1 to 517)

I french-Constant, F.H., Waterfield, N., Burland, V., Perna, N.T.,

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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1 (bases 1 to 519)

1 (Entero-Constant, R. H., Waterfield, N., Burland, V., Perna, N. T., Daborn, P. J., Bowen, D. and Blattner, F. R.

A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bssrfc@bath.ac.uk
his is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
AQ990287
Rfc01035 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01035, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                       Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Ballding, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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AQ990174.1 GI:9648768
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GSS 14-AUG-2000
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                                                                                                                                                           South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Faxil: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTX and mapping to E.
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19: (44) 1225 826621
Fax: (44) 1225 826621
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG02255, genomic survey
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Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Class: shotgun.
Location/Qualifiers

1. 519
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00899"
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                                                                  Department of Biology and Biochemistry University of Bath
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Department of Biology and Biochemistry
University of Bath
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AQ991068 618 bp DNA linear GSS 14-AUG-2000 Rfc01926 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01926, genomic survey
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae; Photorhabdus.
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Rfc02569 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02569, genomic survey
Gaps
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/mol_type="genomic DNA"
/strain="W14"
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100.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
Mismatches
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG02569"
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0;
                                                                14 CTGCTTTTTATACTAACTTG
                                        1 CTGCTTTTTTATACTAACTTG
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Best Local Similarity 100.0
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21; Conservative
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 572)
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Rfc00051 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00051, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
library"
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/clone_lib="Photorhabdus luminescens strain W14 M13
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100.0%; Score 21; DB 28; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 5.2e+02;
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(mol_type="genomic DNA"
/strain="W14"
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                                        organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
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                                                          /mol_type="genomic DNA"
/strain="W14"
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'clone="PLG00051"
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Class: shotgun.
Location/Qualifiers
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location/Qualifiers
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                                                                                                                      clone="PLG02255"
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Photorhabdus luminescens
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AQ989502
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FEATURES
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us-10-082-772b-1.rst

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/db_xref="taxon:29488"
/clone="PLG01579"
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                                                                                                        Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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Best Local Similarity
Matches 21; Conserv
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                          1 (bases 1 to 618)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

farench-Constant, R.H., and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                 Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 82670
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to B. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
              Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Rfc01299 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01299, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
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/organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
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/strain="W14"
/db xref="taxon:29488"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
Tel: (44) 1225 826521
Fax: (44) 1225 826779
Email: bssfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Photorhabdus,
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/ organism="Photorhabdus luminescens"
/ mol_type="genomic DNA"
/ strain="W14"
/ db_xref="taxon:29488"
/ clone="primary phase variant"
/ dev stage="primary phase variant"
/ clone=lib="Photorhabdus luminescens strain W14 M13
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REC01579 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01579, genomic
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
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Efrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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[ tbases I to 678.
[ ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
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                                          AQ990864 linear GSS 14-AUG-2
Rfc01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
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Rfc02132 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02132, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/organism="Photorhabdus luminescens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Enterobacteriaceae; Photorhabdus.
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/strain="W14"
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Class: shotgun.
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1 (Bases 1 to 664)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
Agenomic sample sequence of the entoemopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
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Rfc01864 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01864, genomic survey
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'dev_stage="primary phase variant"
|clone lib="Photorhabdus luminescens strain W14 M13
|library"
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                                                                                                                                                     DB 28; Length 651; Se+02;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
                                                                                                                                                                                                Mismatches
                                                                                                                                                     Score 21;
Pred. No. 5
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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AQ991011.1 GI:9649605
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Search completed: September
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Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photornabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20376633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bssrfc@bath.ac.uk
his is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                               This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTK, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Rfc01894 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01894, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 21; DB 28; Length 675; llarity 100.0%; Pred. No. 5e+02; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:29488"
/clone="PLG02132"
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Photorhabdus luminescens
                                                                                                                                                                                                                                                            Email: bssrfc@bath.ac.uk
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9, 2004, 21:18:21

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 17:33:11; Search time 53.5798 Seconds (without alignments) 2516.866 Million cell updates/sec

Title: US-10-082-772B-2 Perfect score: 243

Perrect score: 243 Sequence: 1 tctgttacaggtcactaata......taaaatcattatttgatttc 243

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 682709 segs, 277475446 residues Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfīles1.seg.* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Appl	1poli	Appli	Appl	App1	App]	App1	Appl	Appl	Appl	Appl	, Appl	ilqq	Appli	Appl	Appl	Appli	Appl	Appl	Appl	Appl	Appl	App	Appli	Appli	Appli	Appl
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		978B	129-	-988A	021-667A-	544-	-785A-18	-702B-50	-013-69	-279-6	268-6	9-896-	397-386-6	1-060	90A	-366A	-404B	-101-	-101-1	-667A	544-1	785A-1	702B-66	532A-6	-886	-886-	-404-	-198-
		1 6	30-92	590-9	21-6	-410-5	28-7	53-7	96-0	82-2	-342-2	10	97-3	308-0	380-090A	16-3	978-4	68-1	68-1	21-6	- 1	- 1	4	- 1	- 1	90-9	04-7	01-1
		08-55	- 1	07-5	08-0	-08-4	08-7	9-4	08-486-	08 - 4	08-3	09-01	- 1	09-3	09-3	09-016	6-80	US-09-068	09-068	08-021	08-410	08-728	09-453	09-107	09-790	09-790	JS-10-204	109-60
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Seguence 8544, Ap	Sequence 7, Appli	Sequence 2779, Ap	П	Sequence 15, Appl	'n	1, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 33, Appl	Sequence 3, Appli		Sequence 39, Appl	Sequence 3, Appli	Sequence 1, Appli	Patent No. 5231168	Sequence 89, Appl
US-09-621-976-8544	US-09-417-485D-7	US-09-134-000C-2779	US-10-204-708-19	US-09-647-390-15	US-08-107-755A-1	US-07-991-867B-1	US-08-544-332-1	US-09-370-861A-1	US-08-487-826B-13	US-09-247-373B-33	US-10-204-708-3	US-09-489-847-38	US-10-204-708-39	US-08-236-754-3	US-08-236-754-1	5231168-1	US-10-204-708-89
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16.5	16.5	16.3	16.3	16.1	16.1	16.1	16.1	16.1	16.1	16.0	16.0	16.0	16.0	15.9	15.9	15.9	15.9
40	40	39.6	39.6	39.2	39.2	39.2	39.2	39.2	39.2	39	39	38.8	38.8	38.6	38.6	38.6	38.6
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ALIGNMENTS

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Sequence 78, Application US/08556978B

Sequence 78, Application US/08556978B

Patent No. 6268169

GENERAL INPORMATION:
APPLICANT: FARNESTOCK, STEPHEN F.
TITLE OF INVENTION: SPIDER SILK ANALOGS
INUMERS OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
CITY: WITTED OF INVENTION: SPIDER SILK ANALOGS
INUMERS OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
CITY: WITTED STATES OF AMERICA
ILMINITON MARKET STREET
CONFITY: UNITED STATES OF AMERICA
ILMIN TYPE: DISKETTE, 3.50 INCH
COMPUTER READABLE PORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER READABLE PORM:
METABORICATION DATA:
APPLICATION NUMBER: US/08/556,978B
FILING DATE: 1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 31,692
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,692
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
TELEPRAX: 302-992-8112
TELEPRAX: 302-992-8112
TELEPRAX: 302-992-8112
TELEPRAX: 302-992-8112
TELEPRAX: SIGNICACION INFORMATION:
TELEPRAX: 302-992-8115
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TELEPRAX: SIGNICACION INFORMATION:
TELEPRAX: 302-992-8115
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6113 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5993 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TAICATITTACGTTTCTCGTTCAGCTTTTTATACTAAGTTGGCATTATAAAAAGCATT
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Patent No. 5434049

GENERAL INFORMATION:
APPLICANT: Ckano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLECTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLECTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7652;
                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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100.0%; Pred. No. 1e-44;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Other nucleic acid; DESCRIPTION: synthetic recombinant plasmid
                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,988A
FILING DATE: 19901001
                                                                                   STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
                                                                Quarles and Brady
                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19901001
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 7652 base pairs NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 7652 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 243; Conservative
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular
                                                                                                                                                     WISCONSIN
                                                                                                                                                                               U.S.A.
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                                                                                                                                   MADISON
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                                                                                                                                                                                               ZIP: 53701
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                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-021-667A-18
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                                                                                                                                                                             COUNTRY:
                                                                                                                                                        STATE:
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                                                                                   2456 TITIACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 2397
                                                                                                                                                        2396 TAICATTTTACGTTTCAGCTTTTTTTTTATACTAAGTTGGCATTATAAAAAGCATT 2337
                                                                                                                                                                                                                                                    2336 GCTTATCAATTIGTIGCAACGAACAGGTCACTATCAGTCAAAAATCATTAGTTGAT 2277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5354 TITIACAGIAITAIGIAGICIGITITITIAIGCAAAAICIAATITAATATATATIAGATATITA 5295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                 121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGCATTGCATTATAAAAAAGCATT 180
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                                           TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Judith W. Zyskind
TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
FILE REFERENCE: ELITRA.012A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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100.0%; Pred. No. 9.9e-45;
iive 0; Mismatches 0;
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Patent No. 5227288
GENERAL INFORMATION: Blattner, Frederick R.
TITLE OF INVENTION: DNA Sequencing Vector with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.012A
CURRENT APPLICATION NUMBER: US/09/630,929
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09630929
Patent No. 6620585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5174 TTC 5172
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US-09-630-929-4/C
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LENGTH: 6043
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US-07-590-988A-1
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
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Best Local Similarity 100.
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
ANTI-SENSE: NO
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APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: Okanora, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pensylvania Ave., NW
CITY: Washington
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                        COMPUTER KEADABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: TELEVALION NUMBER: 20,178
REGISTRATION NUMBER: 20,178
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELEFAX: 202-828-0300
TELEFAX: 202-828-0300
TELEFAX: 202-828-0300
TELEFX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 144; Conservative 0; Mismatches 0;
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AAAATAAAATCATTATTTGATTTC 243
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HYPOTHETICAL: YES
ANTI-SENSE: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NUMBER OF SEQUENCES: 18
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                                                                                    CITY: Wa
STATE: D
COUNTRY:
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OCCAMPITES SYSTEM: PC-DOS/MS-DOS
OFFRANTA SYSTEM: PC-DOS/MS-DOS
OFFRANTA APELICATION NUMBER: 08/08/420,544

CURRENT APELICATION NUMBER: 08/08/420,544

APPLICATION NUMBER: 08/021,667

PELINGS PARE: 04-15-1993
ATTORNEY APERICATION NUMBER: 08/021,667

PELINGS PARE: 04-15-1993
ATTORNEY APERICATION NUMBER: 08/021,667

ATTORNEY APERICATION NUMBER: 08/021,667

ATTORNEY APERICATION NUMBER: 08/021,667

PELINGS PARE: 04-15-1993
ATTORNEY APERICATION NUMBER: 08/021,667
ATTORNEY APERICATION NUMBER: 08/021,667
ATTORNEY APERICATION NUMBER: 08/03/199
ATTORNEY APERICATION NUMBER: 08/
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Score 104.6; DB 4; Length
Pred. No. 1.4e-14;
0; Mismatches 24; Indels
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Digo
STATE: California
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          NAME: Seay, Nicholas J.
REGISTRATION UNDRER: 27386
REFERENCE/DOCKET NIMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-09-453-702B-50
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APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/POCKET NUMBER: 3-UC 1206
TELECOMMUNICATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38562 TGGGTTTTGCTGTTTCGCGTTCA 38584
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APPLICATION NUMBER: US/08/486,013
                                                                                       TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.2%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 70 CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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SOFTWARE: Patenti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-08-486-013-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGGCATTATAAAAAGCATIGCTIATCAATTIGTIGCAACGAACAGGTCACTATCAGTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Welch, Rod TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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ZIP: 53701-2113

COMPUTER READABLE PORM:
MIDDIUM TYPE: DISKETTE, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
FRIOR APPLICATION SATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.3%; Score 144; DB 1; I Best Local Similarity 100.0%; Pred. No. 2.6e-23; Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-666
TELEFAX: 703-312-666
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANBENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
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FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,544
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burland, ...
                                                                                                                                                NAME: Terry, David T. REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burna, Nicc-
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                           TYPE: ......
STRANDENES: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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; ANTI-SENSE: NO
US-08-728-785A-18
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US-09-453-702B-50
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38502 TITICIAGCATIAIGCAGICIAITITITIAGACIAAAIGCALIGIAAIACAITGAIATIAI 38561
                                                                                                                                                                                                    1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                   Gaps
                                                .,0
DB 4; Length 38584;
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Fatent No. 5731149
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TILE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TILLE OF INVENTION: of Their Use
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Matches 101; Conservative
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                                                                                                                                                                                                      Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-08-482-279-69
; Sequence 69, Application US/08482279
; Patent No. 5840498
; GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  468 AACAGGICACTAICAGICAAAAIAAAICAITAIIIIIIII
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                         Score 100.4; DB 1.
Pred. No. 9.6e-14;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRING PATE:
PRING PAPEL
PRING APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-UC 1206
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 69
SEQUENCE CHARACTERISTICS:
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
                                                                                                                                                                                                           41.3%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2408 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                     Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                            linear
                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                          142 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 201
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                                                                                        408 CIGCITITITATACTAAGTIGGCATTATAAAAAGCATIGCITATCAATTIGITGCAACG 467
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Gaps
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                                                                                                                                                                                                                                                                                    Sequence 69, Application US/08342268
Patent No. 5844072
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OBJECT OF INVENTION:
APPLICANT:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Indels
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                                                                                                                                     202 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100.3,
Pred. No. 9.6e-14;
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAX-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
TOPOLOGY:
US-08-342-268-69
                                                                                                                                                                                                                                                   RESULT 10
US-08-342-268-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
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RESULT 11 US-09-015-968-69

41.3%; 99.0%;

Query Match Best Local Similarity

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408 CIGCITITITATACTAAGTIGGCATTATAAAAAAGCATIGCTIATCAATTIGTIGCAACG 467
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Patent No. 6395963
GENERAL INFORMATION
APPLICANT: O'NI, Stephan
APPLICANT: Van Der Lee, Frederique
APPLICANT: Goddijn, Oscar
APPLICANT: Klap, Joke
APPLICANT: Simons, Peter
ITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
FILE REFERENCE: MOG 57680
CURRENT APPLICATION UNBER: US/09/308,090
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2408;
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                                                                                                4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NOMBER: US/09/015,968
FILING DATE: 07-00N-1995
FILING APPLICATION NUMBER: US 08/482,279
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
FILING DATE: 14-AUG-1992
FILING DATE: 26-NAY-1992
ATTING DATE: 26-NAY-1992
ATTING DATE: 26-NAY-1992
ATTING DATE: 26-NAY-1992
ATTING DATE: 26-NAY-1992
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                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/no/?*

CIRCUTING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                     Flores
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLODBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.3%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                     92122
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US-09-397-386-69
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US-09-308-090-1
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US-09-397-386-69
US-09-397-386-69
; Sequence 69, Application US/09397386
; Patent No. 6300470
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Of Their Use
Sequence 69, Application US/09015968

Patent No. 6057425.

GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 AACAGGICACTAICAGICAAAAIAAAAICAITAITIGAITIC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                                                                                                                                                                                                                                ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
FILING DATE:
CLASSIFICATION:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-40N-1995
RICR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
FRICR APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-NG-1992
FRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: CAMPANION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC
TELECOMMUNICATION INPORMATION:
TELEPRONE: (619) 535-9001
TELEPAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 99.0%;
Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-09-015-968-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
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420 CTGCTTTTTTTTTTATACTTGCCATTATAAAAAGCATTGCTTTGTTGCAACG 479
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                                                                                                                                                                                                                                                                                                                                                                               41.3%; Score 100.4; DB 4; Length 3484; 99.0%; Pred. No. 9.9e-14; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65

CORRESPONDENS: 65

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
SIREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 3481.3484
CTHER INFORMATION: /codon_start= 3482
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                                           ORIGINAL SOURCE: ORIGINAL SATADIDOPSIS thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B0801/7093
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APPLICATION NUMBER: 60/037,090
FILING DATE: 05-F8B-1997
ATTORNEY/AGENT INFORMATION:
                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13:
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COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 101; Conservative
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketu
                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                            STRAIN: C24
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                                                                                                                                                                                                                  FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                            Length 3484;
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MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRNT APPLICATION DATA:
APPLICATION NOWBER: US/09/380,090A
FILING DATE: 17-May-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GODDIJN, Oscar
KLAP, Joke
TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 521
                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                       Query Match 41.3%; Score 100.4; DB 4 Best Local Similarity 99.0%; Pred. No. 9.9e-14; Matches 101; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/06472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OHL, Stephan Andreas
SIJMONS, Peter Christiaan
KLEIN-VAN DER LEE, Frederique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-NOV-1997
APPLICATION NUMBER: B9 96203213.2
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: SYN-010 TELECOMMUNICATION INFORMATION:
EARLIER APPLICATION NUMBER: PCT/EP97/06472
EARLIER FILING DATE: 1997-111-18
EARLIER APPLICATION NUMBER: EP 96203213.2
EARLIER FILING DATE: 1996-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 526-6000 TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09380090A
Patent No. 655529
GENERAL INFORMATION:
APPLICANT: OHL, Stephan Andre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3484 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: United States
                                                                                                                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (3482)..(3484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marianne
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US-09-380-090A-1
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US-09-016-366A-13
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3757;	0;
Length 3757;	Indels
B 2; 14;	; ;
41.3%; Score 100.4; DB 2; 99.0%; Pred. No. 9.9e-14;	0; Mismatches
41.3%;	ative
milarity	Conserva
atch cal Si	101
Query Match Best Local Similarity 99.0%;	Matches

Search completed: September 9, 2004, 21:21:18 Job time : 55.5798 secs

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September 9, 2004, 15:48:15 ; Search time 1677.36 Seconds (without alignments) 6279.120 Million cell updates/sec
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243
1 tctgttacaggtcactaata......taaaaatcattatttgatttc 243
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                          Sequence:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	2113 2113 11 Bč 1000	21 Ma 5932	M17028	0	3 AF271663 Clonin	8 U13848 DI	52 AF17845	AX113748 S	AX113749	AAII3/46	AR399301 Sequence	AX370644	7 AX113747	51 AF178451 Integr	U39284 U39285	G U39286 Cloning	92 U37692 Cloning	J02459 Ba	AX092116	3723 AY04872	AY048716 AY048716 CKIM DIAS	3740 AY04874	0267 AY15026	AY05437	AY15026	AY15026	AY15026	AY05437	AY15026	50266 AY15026	AY04871	48714 AY04871	348739 AY04873	63380 BD263380	63379 63379 BD263379
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RESULT 1

	43 bp	DNA	linear	PAT 21-MAR-2001
Sequence 2 from Patent WO(116345.			
AX092113				
AX092113.1 GI:13444356				
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Bacteriophage lambda				
Bacteriophage lambda				
Viruses; dsDNA viruses, no	RNA stag	je; Caudo	virales;	Siphoviridae;
Lambda-like viruses.				
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Droege, P.				,
Sequence-specific dna reco	mbination	ı in euka	ryotic ce	118
Patent: WO 0116345-A 2 08-	MAR-2001;			
	AX092113 Sequence 2 from Patent WOO AX092113. AX092113.1 GI:13444356 Bacteriophage lambda Bacteriophage lambda Viruses, deshway viruses, no Lambda-like viruses. 1 Sequence-specific dna recc Patent: WO 0116345-A 2 08-	AX092113 Sequence 2 from Patent W00116345. AX092113.1 GI:13444356 Bacteriophage lambda Bacteriophage lambda Viruses, dsDNA viruses, no RNA staglambda-like viruses. Sequence-specific dna recombination Patent: W0 0116345-A 2 08-MAR-2001,	AXO92113 Sequence 2 from Patent W00116345. AXO92113 AXO92113.1 GI:13444356 Bacteriophage lambda	. cag

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PAT 10-APR-2001
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                                     240
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Bolanales, Solanaceae, Nicotiana.
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hydroxysteroid sulforransferase subunit.
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
   139 TATCATTITACGITITCICGTICAGCITITITATACTAAGTIGGCATTATAAAAAAGCATT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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100.0%; Pred. No. 7.3e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                                                  DNA
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1. 610
/organism="Nicotiana tabacum"
/do_type="unassigned DNA"
/db_xref="taxon:4097"
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Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
                                                                                                                                                                                                                                                                                              Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                               AX101000 610 bp
Sequence 1 from Patent WO0121780.
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                                                                                                                                                                                                                                                              GI:13619857
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AX101000
LOCUS
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site-specific recombination.
Bacteriophage lambda
Bacteriophage lambda
Bacteriophage lambda
Wiruses; dsDNA viruses.
Viruses; dsDNA viruses.
1 (bases 1 to 361)
Schmeissner, U., McKenney, K., Rosenberg, M. and Court, D.
Removal of a terminator structure by RNA processing regulates int
                                                                                                                                                                                                                     TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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Location/Qualifiers
                                           /organism="Bacteriophage lambda"
/mol_type="unassigned DNA"
/db_xref="taxon:10710"
                                                                                                                            Score 243; DB 6;
Pred. No. 8.9e-34;
0; Mismatches 0;
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/db_xref="taxon:10710"
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J. Mol. Biol. 17
84242838
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Best Local Similarity
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PI PI

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Denstra, R., d'Auriol, L., Andrieu, B., Le Bras, J. and Galibert, F. Cloning and sequencing of Plasmodium falciparum DNA fragments containing repetitive regions potentially coding for histidine-rich proteins: identification of two overlapping reading frames Blochem. Blophys. Res. Commun. 146 (1), 368-377 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TATCATTITACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 180
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                                                                                                                                                                                                                                                                         PI SIGRID SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC
C12N15/09, AG1K31/711, AG1K48/00, AG1P25/00, AG1P25/28, C07H21/04, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/121, C12N5/10, C12P21/08 PC
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                                                                                                               OS Rattus norvegicus (rat)
PN 4D 2002512772-A/49
PD 08-MAY-2002
PF 05-FEB-1999 JP 2000530634
PR 09-FEB-1999 US 60/074135,12-FEB-1998 US 60/074518
PAUL, F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, ROHINI KUNER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histidine-rich protein.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum (malaria parasite P. falciparum)
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

| (bases | 10.2758)
Scheek, S., Nikolich, K. and Zhukovski, E.
Immediate early gene and method for using the same
Patent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: P.falciparum, cDNA to mRNA, clone M4 Location/Qualifiers
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SIGRID SCHEEK, KAROLY NIKOLICH, EUGENB ZHUKOVSKI
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Best Local Similarity 100.0%; Pred. No. 5.9e-34;
Matches 243; Conservative 0; Mismatches 0;
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Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Location/Qualifiers
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PC C12N15/00,C12N5/00
CC n is either a, t, g,
FH misc feature (1).
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GSWFDHIHGWMPMREKKNFLLLSYBELKQDTRRTVBKICQFLGKTLBPELNLILKNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MSDDFLWFEGIAFPNMGFRSETLRKVRDEFVIKDEVIILTYPK
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                                                                                                               ogura, K. Dhrect Submission Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of Pharmacy and Life Science, Department of Drug Metabolism and Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392, Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518, Fax:+81-426-76-4517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332
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                       Ogura, K., Satsukawa, M., Kato, K., Okuda, H. and Watabe, T.
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAGCTTGGCATTATAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
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Sciurognathi; Muridae; Murinae;
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Worley, P.F., Lanahan, A., Goetz, B., Hiemisch, H., Kuner, R.,
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Pred. No. 6e-34;
Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                   organism="Macaca fascicularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hydroxysteroid
/protein_id="BAA12823.1"
                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="liver"
/clone lib="lambda gtll"
511. .1468
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Immediate early gene and method
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BD225922.1 GI:33035702
JP 2002512772-A/49.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Cr
Mammalia; Eutheria; Rodentia; So
                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:1345406"
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                                                                                                                                                                                                                                                                                                                                                                                 clone="monHST-1"
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                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
         (bases 1 to 1668)
                                                                                             (bases 1 to 1668)
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BD225932/c
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/translation="wimitpsaqltlikgnkswvpgppskstvsislisnscspddpl
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artdrpsqqlrslngewltrpvaah"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MEKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
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ANMDNFFAPVFTYQGBKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                  SYN 20-JUL-2000
                                                                                                                                   2368 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTATTTGAT 2309
                                                                                                                                                                                                                                                                                                                  AF178449 3485 bp DNA linear SYN 20-JUL-2(
Integration vector pCD11PKS chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
AF178449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="attp; attachment site from bacteriophage lambda"
complement(1327. .1986)
/gene="cat"
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-AQG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (Dases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome plasmid 43 (1), 12-23 (2000)
                                             2428 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                          GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
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trans1_table=11
product="beta-galactosidase alpha peptide"
(db_xref="G1:9294786")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'producE="chloramphenicol transacetylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Integration vector pCD11PKS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="Escherichia coli"
1. .385
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pCD11PKS
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'transl_table=11
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/product="histidine rich protein B"
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/db_xref="G1:160341"
/translation="MINHXPHYFHRHHINHHIXHRHHHHHHHHHHHHHHHHHINHHQILHQN RRQIHQILLSINNKIMGYAIFLFISILLHLIVYLVIHRL"
                                                                                                                                                                                                                                           /translation="DPYKERIKSDIRQINESQYLKSLAYKYISGEDYTQYLLINEVLK
DDQDYCTCTRRTIYESMDNTVEFAKKMYELSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MYLFIYIFFFFFFFFFVIVQKDIEQLDIKCAHEQMNIQKQYDE
KKKPLFEKRDEIIQKIPGFWANTLRKHPALSDIVPEDIDILNHLVKLDIKDNMDNNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKITEIFGEKAKEFMEDLTLVKHVTFDNNQEKVVECTRIKWKEGKNPIAAVTHNRSDL
DNEIPKWSIFEWFTTDELQDKPDVGELIRREIWHNPLSYYLGLEEFDEFDDFFDEEFD
DDDDDDDDDDDDDDDDFKDDLDGDDGNNDDNDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MVLVTCNRALAQGDFCLLALIFCHQTCRTPEKHKASQSSAKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="PQYQFVGAKLFRWWCWRRRGWRRRWWLVIKLMLIETSFALDCEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2548 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2141. .2650)
/note="putative VECTOR sequence Bacteriophage lambda
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protein_id="AAA29621.1"
db_xref="G1:160343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="histidine rich protein D"
protein_id="AAA29622.1"
db_xref="G1:160344"
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                                                                                                                                                                              protein A"
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/organism="Plasmodium falciparum"
/mol type="genomic DNA"
/db_xref="taxon:5833"
1. .234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="histidine rich protein
protein id="AAA29620.1"
db_xref="GI:160342"
                                                                                                                                                                                                                                                                                                         gene="histidine rich protein B" 124. 1072
gene="histidine rich protein B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (828. .1589)

Ganea-Whistidine rich protein B"
complement (828. .1589)

/gene="histidine rich protein B"
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/gene="histidine rich protein C"
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/gene="histidine rich protein C"
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100.0%; Pred. No. 5.4e-34;
iive 0; Mismatches 0;
                                                                                          Ę,
                                                                                                                                   gene="histidine rich protein A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2596. .2758)
/gene="histidine rich protein D"
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                                                                                          gene="histidine rich protein
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                                                                                                                                                            codon_start=1
product="histidine rich
                                                                                                                                                                                                /protein_id="AAA29618.1"
/db_xref="GI:160340"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                         324. .1072
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SLIWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
                                                                                                                               /transI_table=11
/product="beta-galactosidase alpha peptide"
/protein_id="AAF86672.1"
/db_xref="GI:9294789".
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 243; DB 12; 100.0%; Pred. No. 5.2e-34;

    4105
/organism="Cloning vector pLDR9"

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                                                                                                                                                                                                                                                         2972. .3081
/note="multiple cloning site"
                                                                                                                                                                                                                                           ARTDRPSQQLRSLNGEWLTRPVAAH"
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:130501"
216. .1031
                                                                                .3137)
                                                  complement (2754. .3137)
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1 (bases 1 to 4105)
                                                                                complement (2754.
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/transT_table=11
                                                                                               /gene="lacZa"
/codon_start=1
/transT_table=11
                                                                     /gene="lacZa"
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                                                                                                                                                                                                                                                                                                                                                               243; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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VERSION
                                                    gene
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AF271663
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SOURCE
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LKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETF
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                                                                                                                                                                                                       TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                       733 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTGATATTTA 792
                                                                                                                                                                                                                                                                           TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                        793 TATCATTTTACGTTTCTCGTTCAGCTTTTTATACTAAGTTGGCATTATAAAAAGCATT 852
                                                                                                                                                                                                                                                                                                                                                               GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAAATAAAATCATTATTGAT 912
                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF178450 10-JUL-20 JARS bp DNA linear SYN 20-JUL-20 Integration vector pCD11PSK chloramphenicol transacetylase (cat) and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iowa State University, 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668. .915
/note="attP; attachment site from bacteriophage lambda"
complement(1327. .1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequences; vectors.

1 (bases 1 to 3485)
Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
                                                                                                                                    TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                             GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAAAAATCATTATTTGAT
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0
                                                                  Length 3485;
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State Us
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transacetylase"
                                                                                                    Indels
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/organism="Integration vector pCD11PSK"

/mol_type="genomic DNA"

/db_xref="taxon:106603"

/lab_host="Escherichia coli"

1. .385
                                                                100.0%; Score 243; DB 12;
100.0%; Pred. No. 5.2e-34;
tive 0; Mismatches 0;
2972. .3081
/note="multiple cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transT_table=11
/product="chloramphenicol
/protein_id="AAF86673.1"
/db_xref="GI:9294790"
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Integration vector pCD11PSK
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                                                                                                  Conservative
                                                                                  Similarity
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Best Local Simi
Matches 243;
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AF178450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circular SYN 11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCATTTTACGTTTCTCGTTCGGTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      673 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     793 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02139,
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Submitted (24-mAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA
Location/Qualifiers
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IELDLINSGKILESFRPERFPPMSTFRVILCGAVLSRIDAGGEGLGRRIHYSGNDLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/note="Multiple Cloning Site (MCS); contains unique sites /note="Multiple Cloning Site (MCS); contains unique sites complement(2155. .2174)
/gene="T7 RNA polymerase"
complement(2155. .2174)
Malone, J. A.

Direct Submission

Direct Submission

Submitted (19-AuG-1994) James A. Malone, International Technical
Submitted (19-Aug-1994) James A. Malone, International Biotech
Services, Molecular Biology Reagents Division, Pharmacia Biotech
Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA

Location/Qualifiers
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the first base of the newly synthesized single strand"
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3932. 3947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="lac operator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001. .2007
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                                                                                                                                                                                                                                                        gene="bla"
                                                                                                                                                                                                                                                                                                      gene="bla"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2677 TITTACAGTATTARGTGTGGTGTTTTTTTATGCAAAATCTAATTTAATATATTGATATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U13848.1 GI:595702
T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide,
attP.
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                                                                                                                                                                                                                                                                                                                                                                                      complement(1992. .2258)
/note="hypothetical 9.2 kD protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified cloning vector
unidentified cloning vector
artificial sequences; vectors.
1 (bases 1 to 4190)
                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1
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pExCell cloning vector,
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trans table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Best Local 8
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XXU13848/c
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VERSION
KEYWORDS
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VLERPPPRWSSNSPYSESYYARSIAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF178453 4549 bp DNA linear SYN 20-JUL-2000
Integration vector pCD13FSK aminoglycoside adenyltransferase (aadA)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
AF178453
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Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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                                                                                                                                                                                                                                                                                                                100.0%; Score 243; DB 12;
larity 100.0%; Pred. No. 4.9e-34;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                    4038. .4145
/note="multiple cloning site"
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/db_xref="taxon:106606"
/lab_host="Escherichia c
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                                      complement (3818.
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                                                         /gene="lacza"
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/db_xxef="G1:9294796"

/translation="MIWASNDVTQQSSRPKTKINIMREAVIAEVSTQLSEVVGVIERH
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VTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLASRADQLEEFVHYVKG
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complement(1798. .2652)
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                                                                               1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                        Gaps
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, Score 243; DB 12; Length 4190;
Pred. No. 5e-34;
0; Mismatches 0; Indels 0;
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
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/lab_host="Escherichia coli"
1. 385
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Integration vector pCD13PKS
artificial sequences; vectors.
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    100.0%;
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100.0%; Pred. No. 4.7e-34;
ative 0; Mismatches 0;
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Patent: WO 0127322-A 14 19-APR-2001,
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 14 from Patent WO0127322.
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                                                                  /note="pJMF3"
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synthetic construct
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Matches 243; Conservative
   1. .5641
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Chitobiase as a reporter enzyme
Chitobiase as a reporter enzyme
Patent: WO 0127322-A 13 19-APR-2001;
Blitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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WO0127322.
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4861 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 4802

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Chitobiase as a reporter enzyme
Patent: WO 0127322-A 11 19-APR-2001;
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. 5826
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                                                                                                                          DNA
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Sequence 11 from Patent W00127322.
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AX113746.1 GI:13939913
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synthetic construct
artificial sequences.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Length 248; Indels

Score 243; DB 8; Pred. No. 1.8e-40;

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TTC 243 TTC 248

185

TATCATTITACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATT 180

TATCATITITACGITITCTCGTTCAGCTTTTTTATACTAGGTTGGCATTATAAAAAAGCATT GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT

TITTACAGIATIAIGIAGICIGITITITIAGCAAAATCIAATITAATATATATATATITIA

TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

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ACC44676 standard; DNA; 282
                   Query Match
Best Local Similarity 100.
Matches 243; Conservative
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                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                              Gaps
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                                                                          0;
                                        Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinase lambda integrase attP DNA recognition sequence.
                                                                          Indels
74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
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                                  Score 243; DB 4;
Pred. No. 1.8e-40;
                                                                        0; Mismatches
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                                      100.08;
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                                                                          Conservative
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 Sequence 243
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                                    Query Match
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Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a eukaryotic chromosome (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel eukaryotic chromosome comprising one or many att sites which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                            Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindenbaum M,
J;
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   (first entry)
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Shellard
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29-MAY-2003
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                                                                                                                                                                                                                                                                                     Synthetic
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Stewart S
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The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification of the invention

German.

Disclosure; Page 35; 164pp;

Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;

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introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic
                                                                                                                                                                                                                                                                                        o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                             cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
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blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
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can be used in gene therapy. (M1) is useful
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                                                                                                                                                                                   exemplification of the present invention
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Matches 243; Conservative
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chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, trNA, rDNA, structural proteins, marker proteins, ligands, receptors, ibozymes, therapeutic proteins, and proteins, ligands, receptors, ibozymes, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (RAC). This producing plant artificial chromosomes of the invention
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Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
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                                                                                                                              invention relates to a novel method for producing plant artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
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                                                                                    Disclosure; Page 263-264; 269pp; English.
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Matches 243; Conservative
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Meyer P,

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The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 DNA for use in the material of the invention. The principal of the invention of sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or polymer applied on it. The printed material is useful in a method for synthesising DNA where the product of samplification and/or ligation is constantiation of nucleotide insertion/deletion, single nucleotide collympthism (SNP) and sequencing analysis, in a diagnostic method for determination of nucleotide insertion/deletion, or SNP analysis.

Optionally, the cDNA and/or full-length cDNA is useful for the peptide, optionally the cDNA and/or full-length cDNA is useful for the peptide, optionally applications, or for providing scientists with oligomer and/or polymers from the printed materials easily and immediately. From the printed materials and/or polymer and/or the polymers from the printed materials as all/or polymers can be obtained printed materials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTATTTGAT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immediately and directly, without need to make a request for it. The oligomers and/or polymers can be delivered and stored easily with reduced labour and time while eliminating the need to use special equipment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             808 rererracaderearracearerrandingarrearagreerecarardrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGCTTGGCATTATAAAAAGCATT
                                                                                                                                           Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rtrtacagrarrangragrergritritriaggaaaneraarritaaratarraarrara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     facilities. Thus, the printed material is a quick, efficient and inexpensive sample delivery system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 243; DB 7; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligomer storage; oligomer delivery; ds.
                                                                                                                                                                                                                                                Example 1; Page 31-32; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 243; Conservative
                                                                                                  WPI; 2003-354676/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 TTC 1050
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                                              Hayashizaki Y;
(RIKE ) RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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X X X B X B X B X B X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                              The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibbotic resistance. The present sequence is the attb coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
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                                                                                                                                                                                               Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGGTTGGCATTATAAAAAAGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTATCAATTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R. amplify, lambda phage, printer material, insertion,
single nucleotide polymorphism, sequencing, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 243; DB 5;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ80306 standard; DNA; 1469 BP.
                                                                                                                                                                                                                                                                                                  Claim 8; Fig 3D; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lambda fragment in plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
  99GB-00021937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2002; 2002WO-JP009766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 243; Conservative
                                                                                                                                                   WPI; 2001-266072/27
                                                 (UYLE-) UNIV LEEDS
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                                                                                                  Zubko E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 TTC 381
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  17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR;
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Query Match

Best Loca Matches

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ACC44716 standard; DNA; 4346 BP.
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TTC 189
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                      WO9940225-A1
                                                                  05-FEB-1999;
                                                                                     09-FEB-1998;
12-FEB-1998;
                                                                                                                                                       Worley PF, 1
Nikolich K,
                                            12-AUG-1999
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                                                                                                                                                      Worley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ID ACC4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           988 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATCATTITACGITICICGITICAGCITITITATACTAAGTIGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                        oligomer and/or polymer applied on support. The support has oligomer and/or polymer applied on it, and is in the form of loose-leaf sheet or card. The support is useful for storing and/or delivering an oligomer and/or polymer applied on it. The present sequence is Bacteriophage lambda DNA used in the exemplification of the invention
                                                                                                                                                                                             New support useful for storing and/or delivering an oligomer and/or polymer applied on support, has oligomer and/or polymer applied on it, and a loose-leaf sheet or a card.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                          1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATTTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   928 TATCATTTACGTTCTCGTTCAGCTTTTTATACTAGGTTGGCATTATAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immediate early gene; IEG; neuron; brain; function; growth factor;
transcription factor; signal transduction; cytoskeletal protein;
metabolic enryme; learning; memory; synaptic transmission; tolerance;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                              The invention relates to a method for storing and/or delivering an
                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                              ; Score 243; DB 7; Length 1469; Pred. No. 1.9e-40; 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                         Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat neuronal immediate early gene cDNA clone R280.
                                                                                                                                                                                                                                       Example 1; Page 30-31; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                              05-NOV-2002; 2002WO-JP011492.
                                                                                    05-NOV-2001; 2001JP-00339217
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 243; Conservative
                                                                                                        (RIKE ) RIKEN KK.
(DNAF-) DNAFORM KK.
(HAYA/) HAYASHIZAKI Y.
Bacteriophage lambda
                                                                                                                                                                          WPI; 2003-441569/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1048 TTC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TTC 243
                   WO2003040360-A1
                                                                                                                                                    Hayashizaki
                                          15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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clone R280. An IEG is a grimulus e.g., neuronal stimulation. Such immediately following a stimulus e.g., neuronal stimulation. Such meronal IEGs have been found to encode a variety of proteins, including transcription factors, cytoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in, for example, learning, memory, synaptic transmission, tolerance and neuronal plasticity. Neuronal IEGs, neuronal IEG protein products, cells expressing neuronal IEGs, neuronal IEG proteins can be used to treat an animal with a deficiency is minimised. The costimuli, such that the effect of the deficiency is minimised. The costimuli, such that the effect of the deficiency is minimised. The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IEGs and products are useful in identifying compounds that modulate the expression or are useful in identifying compounds that modulate the expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating conditions related to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCATITITACGITICICGITCAGCITITITIAIACIAAGITGGCALTAIAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 TITTACAGIATIATGIAGICIGITITITAIGCAAAAICTAAITTAATATATATATATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 TATCALTITACGITICICGITICAGCITITITATACTAAGITGGCATIATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents rat neuronal immediate early gene (IEG) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                           Scheek S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful in identifying compounds that modulate the exactivity of IEG nucleic acids or proteins, respectively
                                                                                                                                                                                                                                                                                       Kuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.96-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel genes and polypeptides, useful for treatir
deficiency in nIEG responsiveness to a stimulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 243; DB 2; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                       Hiemisch H,
                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE (BADI ) BASF-LYNX BIOSCIENCE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 114-115; 134pp; English.
                                                                                                                                                                                                                                                                                       Goetz B,
                                                                                                                                                                                                                BASF-LYNX BIOSCIENCE AG
99WO-US002462
                                                                   98US-0074135P
98US-0074518P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243; Conservative
                                                                                                                                                                                                                                                                                       Lanahan A,
Zhukovski
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4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 4249
                               GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 240
                                                     4250 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAAATAAAATCATTAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perkins E;
                                                                                                                                                                                                   BP.
                                                                                                                                                                                                   ABT16615 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2002; 2002WO-US017451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001US-0294687P. 04-JUN-2001; 2001US-0296329P.
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-140436/13.
                                                                                                                        TTC 4312
                                                                                            TTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200296923-A1
                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                              03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-2002.
                                 181
                                                                                                                        4310
                                                                                                                                                                                                                               ABT16615;
                                                                                            241
                                                                                                                                                                     RESULT 10
                                                                                                                                                                                   ABT1661
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                                                          g
                                                                                          \delta
                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of almoda-integrase. Also described: (I) a platform artificial chromosome catalysed recombination; and (2) a method (MI) for in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome, preferably an ACes. (II) is useful for producing a retificial chromosome, preferably an ACes. (II) is useful for producing a ratificial chromosome, preferably an ACes. (II) is useful for producing or artificial chromosome, preferably an ACes. (II) ipid-mediated transfection by a carrier system, microinfection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4070 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4130 TITITACAGTATITATGTCTGTTTTTTTATGCAAAATCTAATTTAATATTGATATTTA 4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAGTTGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITIACAGIAITAIGIAGICIGITITITAIGCAAAAICIAAITIAATAITATATTIA 120
                                                                                                          Chromosome.based platform, artificial chromosome, eukaryotic chromosome, att site; integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                               Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4346;
                                                                                                                                                                                                                                                                                                                                                                                     Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 243; DB 7;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                     Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 244-245; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                        (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                     Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                               30-MAY-2002; 2002WO-US017452
                                                                                                                                                                                                                                                                                                             2001US-0294758P
                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002US-0366891P.
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Perez C, Li
Shellard J;
                                                                                                                                                                        Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-140461/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                   WO200297059-A2.
                                                                                                                                                                                                                                                                                                             30-MAY-2001;
                                                 29-MAY-2003
                                                                                                                                                                                                                                                 05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                   Perkins E,
Stewart S,
                                                                                                                                                                                     Synthetic
                    ACC44716;
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                                                                                                                                                                                                                                                                                                                                                                                                   Stewart
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Matches
      ВÞ
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting chromosomes. The invention also relates to methods for targeting conserving the heterologous DNA into plant artificial chromosomes. The for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ENNA, ENNA, structural proteins, marker proteins, liquads, receptors, ribozymes, therapeutic proteins, and control factors, antigens, hormones, crokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters contrologous nucleic acid is contained within a bacterial artificial chromosome (BAC). This properties are represented the DNA of a plasmid used in the marked of the plant of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                      Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
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Artificial plant chromosome related plasmid DNA SEQ ID No 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 19; Page 255-256; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
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protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF30800;
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                                                                                                                                                                                                                                                                                                                                                                          TITIACAGTATTATGTAGTCTGTTTTTTATGCAAATCTAATTTAATATTGATATTTA 4189
                                                                                                                                                                                                                                                                                                      TATCATTITACGTTTCTCGTTCAGCTTTTTTATACTAGGTTGCCATTATAAAAAGCATT 4249
                                             ö
                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                       TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTGATATTTA 120
                                                                                                                                                                                                                                                             TAICATTITACGITICTCGTICAGCTTTTATACTAAGTTGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider, dragline protein, variant, monomer, polymer, circular, fibre forming region, Spidroin 1, Nephila clavipes, DP1, mimic, DP-1A analogue, fibre, high tensile strength, elasticity, clothing, rope, surgical suture, implant, reinforcement, film, coating, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the complete nucleotide sequence of the plasmid pAl26i. This plasmid was used in the construction of the vector pFP510 which was used to express synthetic spider dragline variants, DP-1A.9 and DP-1B.9. pAl26i comprises a replication origin active in E. coli, a
                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP-18.9. pAL261 comprises a replication origin active in E. coli, a selectable genetic marker which is a gene conferring resistance to ampicillin, sites for the restriction endonucleases BamHi and BglII with no essential sequences between them, and a third respriction site for PstI, located within the selectable marker which produces cohesive ends incompatible with those produced by BamHI and BglII. The polypeptide monomers are variants based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. Synthetic analogues of DP1
                                                                                                                                                                                                                                                                                                                                                 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells.
                                                                                   TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                             Gaps
                                             .,
                                           Indels
                                        0;
                    Pred. No. 1.9e-40;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 нi
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100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT18924 standard; DNA; 4909 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00077600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                  Local Similarity 100.
1es 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-036479/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTC 4312
                                                                                                                                                                                                                                                                                                                                                                                                                                     TTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pA126i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9429450-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic,
                                                                                                                              4070
                                                                                                                                                                                                                  4130
                                                                                                                                                                                                                                                                                                      4190
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                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT18924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
AAT18924/C
XX
AC AAT189,
XX
DT 17-JAN
XX
DE Plasmic
XX
XX
Spider,
XW
Spider,
XM
Spider,
X
                    Best Loca
Matches
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protein and the pattern of variation among individual repeats. DP-1A malogues are composed of a tandemly repeated 101 amino acid monomer analogues are composed of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus sequence given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence is deleted, so also is the surrounding sequence. Calanine sequence is deleted, so also is the surrounding sequence. Caletions usually encompass integral multiples of three consecutive residues; (4) deletion of GXG is generally accompanied by deletion of GXG in the same sequence; and (5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine residues. The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGTGATATTTA 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITIACAGIAITAIGIAGICIGITITITAIGCAAAAICTAAITITAATAITIGAIATITA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATAAAATTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCATITITACGTITCTCGTICAGCTTTTTTATACTAAGTIGGCATTATAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; LacZ gene; promoter; vector; pJMF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector plasmid pJMF3 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 243; DB 2; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "CAP-CAMP binding site"
1820. .1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function= "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function= "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF30800 standard; DNA; 5641 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1850
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 243; Conservative
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Vibrio harveyi.
Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitobiase; reporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2274
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21-JUN-2001
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Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
                                                                       Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2000; 2000WO-US021048
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                     (revised)
                                                                                                                                    Vibrio harveyi.
Bacteriophage lambda.
                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                             WO200127322-A2
                                                                                                                                                                                                                                                                                                             protein bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-1999;
                                   11-SEP-2003
21-JUN-2001
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                                                                                                                                                                                                                                     -35_signal
                                                                                                                                                                                                                                                                         10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind J;
           AAF30801;
                                                                                                                                                             Chimeric
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4882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4822
                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of vector plasmid pJMF3, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chitobiase gene (see AABD0484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pJMF3. The invention also comprises expression vectors which express the cytoplasmic
                                                                                                                                                                                                                                                                        Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                       form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4703 rererracadereacraaraceareraagragragracaragragragraerarararere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4823 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5641;
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           note= "Lac repressor binding site"
                                                             /product= "lacz-chitobiase fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 243; DB 4;
100.0%; Pred. No. 1.9e-40;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            Example 1; Page 32-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%;
Conservative C
                                                                                                                                      02-AUG-2000; 2000WO-US021048
                        .895. .2014
'*tag= e
 ರ
                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
                                                 /partial
 *tag=
                                                                                                                                                                                                                                     WPI; 2001-290731/30.
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es 243; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4943 TTC 4945
                                                                                                                                                                                                                                                  P-PSDB; AAB20484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TTC 243
                                                                                       WO200127322-A2
                                                                                                                                                               13-OCT-1999;
                                                                                                             19-APR-2001
                                                                                                                                                                                                             Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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*tag= d
'note= "Lac repressor binding site"

.2014

1895.

/partial

'*tag=

"Lac promoter"

.1883

1857.

function=

site"

a "CAP-cAMP binding

.1826

*tag=

Location/Qualifiers

.1810

783.

*tag= note= 1820. . promoter"

"Lac

.1850 function=

845.

υ

*tag=

/product= "lacZ-chitobiase fusion"

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Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of vector plasmid pJMF4, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chitobiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pJMF4. The invention also comprises expression vectors which express the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription within a test sequence, detecting a successful transformation, and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 34~36; 44pp; English.
WPI; 2001-290731/30.
                                                               P-PSDB; AAB20484.
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100.0%; Score 243; DB 4; Length 5670; 100.0%; Pred. No. 1.9e-40;

Best Local Similarity

AAF30801 standard; DNA; 5670 BP.

RESULT 13 AAF30801/c

Query Match

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(revised)
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                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             5130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                       TTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB20485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio harveyi.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200127322-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .3-OCT-1999;
                                                                               243;
                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2001
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                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                          AAF30799;
                                                                                Matches
                                                                                                                                                                                                                                                                                                                                             RESULT 15
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                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene system in that it is not necessary to engineer many host
                                                                                                              TATCATITIACGITICICGTICAGCITITITIATACTAAGTIGGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claimed reporter gene construct comprises pDYK9. The invention relates to genetic constructs and methods of using a cytoplasmic form of chitchiase enzyme as a reporter. The invention also comprises expression vectors which express the cytoplasmic form of chitchiase. Methods are provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of vector plasmid pDYK9, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia colidnah promoter in plasmid pACYC184. pDYK9 was used to assess the regulation of the dnah gene using chitobiase as a reporter enzyme. A
                                                                                                                                 TAICATITIACGITICTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATT
                                                                                                                                                        GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                     TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                             TITIACAGIAITAIGIAGICIGITITITIAIGCAAAAICIAAITITAAIATAGAIAITIA
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Chitobiase; reporter gene; dnaA gene; promoter; vector; pDYK9; ds.
   ;
                                                                                                                                                                                                                                                                                                                                                                 Vector plasmid pDYK6 encoding chitobiase reporter enzyme.
  Indels
  ó.
 0; Mismatches
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                                                                                                                                                                                                                                                                                   AAF30798 standard; DNA; 5826
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 Conservative
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cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5008 TATCATTTACGTTCTCGTTCAGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                       Sequence 5826 BP; 1574 A; 1346 C; 1389 G; 1517 T; 0 U; 0 Other
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                                                                                                                                              Length
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/product= "dnaA/chitobiase fusion"
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                                                                                                                                           100.0%; Score 243; DB 4; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                  0; Mismatches
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2331. .4973
/*tag= a
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The present sequence is that of vector plasmid pDXXII, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia coli rpmH-dnah promoter in plasmid pACYC184. The plasmid encodes a dnah-chitobiase fusion protein (see AAB20485). It was used to assess the regulation of the dnah gene using chitobiase as a reporter enzyme. A calaimed reporter gene construct comprises pDXXII. The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. The invention also comprises expression cotors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter, identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise os field)
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Sequence 6071 BP; 1638 A; 1400 C; 1451 G; 1582 T; 0 U; 0 Other;

0 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG Gaps 0; Query Match 100.0%; Score 243; DB 4; Length 6071; Best Local Similarity 100.0%; Pred. No. 1.9e-40; Matches 243; Conservative 0; Mismatches 0; Indels 0. 셤 $\stackrel{>}{\circ}$

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5372

TTC 243 241

5313

5373 TTC 5375

9, 2004, 18:05:39 Search completed: September Job time : 277.724 secs

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AQ990809 R£C01638
AQ991303 R£C02205
AQ990470 R£C01245
AQ990878 R£C01715
                                                                             6; Search time 1962.91 Seconds (without alignments) 3696.811 Million cell updates/sec
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                                                                                                                                                              1 totgttacaggtcactaata......taaaatcattatttgatttc 243
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                               9, 2004, 17:30:16
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Listing first 45 summaries
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11: gb_htc:*
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Fax: (44) 1225 826779

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227

62

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AQ990470 10.00 769 bp DNA linear GSS 14-AUG-2000 Rfc01245 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01245, genomic survey
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Photorhabdus.
1 (bases 1 to 769)
Efrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
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                                                                                                                                                                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 214.8; DB 28; Length
Pred. No. 6.1e-31;
0; Mismatches 13; Indels
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/organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                   /db_xref="taxon:29488"
/clone="PLG02205"
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Photorhabdus luminescens
bssrfc@bath.ac.uk
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firstch-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W4: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                     /db xref="taxon:29488"
/clone="PLG01638"
/clone="primary phase variant"
/clone lib="Photorhabdus luminescens strain W14 M13
/clone lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
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                   This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Forward Class: shotgun.
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Enterobacteriaceae; Photorhabdus.
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Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 712;
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                                                                                                                                                                                   /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 243; DB 28;
; Pred. No. 2.6e-36;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RH
Biochemistry
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Department of Biology and Bloch
University of Bath
South Building, Bath BA2 7AY, U
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                    Location/Qualifiers
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    Smail: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                            Induct 100.0%;
Local Similarity 100.0%;
Les 243; Conservative 0;
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AQ991303.1 GI:9649897
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                                                                                                                                                                                                                                                                                                                          /note="Genomic DNA from strain W14 was size selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 ITNACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAATITAAIATATATATATATATAT 650
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               This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus
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Photorhabdus luminescens genomic clone PLG01715, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 211.4; DB 28; Length 769;
Pred. No. 2.1e-30;
0; Mismatches 13; Indels 1;
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="W14"
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                                                                                                                                                                                                                             /db xref="taxon:29488"
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                 /clone="PLG01245"
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bssrfc@bath.ac.uk
                                                                                         Seq primer: M13 Forward Class: shotgun.
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Best Local Similarity 94.2%;
Matches 229; Conservative 0
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BQ157398 472 bp mRNA linear EST 24-APR-2002
NF104D07IR1F1062 Irradiated Medicago truncatula cDNA clone
NF104D07IR 5', mRNA sequence.
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                  This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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Fax: 580 221 7380
Email: gdmaymoble.org
Email: gdmaymoble.org
Plate: 104 row: D column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
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97.5%; Pred. No. 6.5e-30;
live 0; Mismatches 4;
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The Samuel Roberts Noble Foundation
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Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:29488"
/clone="PLG01715"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .764
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                    Seq primer: M13 Forward Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ157398.1 GI:20294457
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Best Local Similarity 97.5
Matches 232; Conservative
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/tissue_rype______________/
dev_stage="seedling"
/dov_stage="seedling"
/done_lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2. UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
----1 bwa from each sample. The cDNA was directionally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 TATAAAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ford RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR
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1 (bases 1 to 751)

Éfrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
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Rfc00126 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00126, genomic survey
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100.0%; Pred. No. 1.3e-27;
tive 0; Mismatches 0;
                                                                                                                /organism="Medicago truncatula"
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                  Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                             tissue_type="seedlings"
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                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                 clone="NF092E03IR"
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                                                                                                /clone="Nature" catchings"
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/dev stage="seedlings"
/dev stage="seedling"
/dev stage="seedling"
/clone lib="lirradiated"
/clone lib="lirradiated"
/clone lib="rirradiated"
/clone gy gamma or 0.5.1,5,0 rs 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12,24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Strategene) and
packaged using the Gispack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-ZAP XR vector using ExAssist
helper phage and the B. coli strain XLI-Blue MRF'
(Strategene). Excised plasmids were plated using SOLR
cells."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Fig. Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: S80 221 7391
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NF092E03IR1F1023 Irradiated Medicago truncatula cDNA clone
NF092E03IR 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                 organism="Medicago truncatula"
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Insert Length: 473 Std Error: 0.00
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                                                         mol_type="mRNA"
'db_xref="taxon:3880"
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annotation of identified clones (BLASTX, BLASTN and coli K12 genome) please see ffrench-Constant et al. Acids Res.
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                                                                                                                                               organism="Photorhabdus luminescens"
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                                                                                                                                                                                                                                                                                                                                                                                   .4; DB;
le-25;
                                                                                                                                                                                                                                                                                                                                                                                   Score 186.4;
Pred. No. 1e-2
0; Mismatches
                                                                                                                                                                /mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                     /db_xref="taxon:29488"
/clone="PLG01106"
                                                                                                      Location/Qualifiers
1. .743
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                                                                 Seg primer: M13 Forward
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BY115594.1 GI:26226695
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97.7%;
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                                                                                        Class: shotgun.
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1 (bases 1 to 74)

1 (bases 1 to 74)

1 ffrench-Constant, R. H., Materfield, N., Burland, V., Perna, N.T.,

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence 20378633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 TCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAAC 200
                                                           This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ990346
Rfc01106 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 IGTTITITATGCAAAATCTAATTTAATATATATGATATTTANATCATTTTACGTTTCTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 CCATCTAAGTAGTTCATAGTGACTGCATATGTTGTTGTTTTACAGTATTATGTAGTC
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826721
Fax: (44) 1225 826729
Banil: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%; Score 187.4; DB 28; Length 751; 95.5%; Pred. No. 6.7e-26; ive 0; Mismatches 8; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACAGGICACTAICAGICAAAAIAAAAICAIIAIIIGAIIIC 243
                                                                                                                                                                                                                 /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:29488"
/clone="PLG00126"
                                                                                                                                                                                Location/Qualifiers
    Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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Photorhabdus luminescens
                                                                                                                                             Seq primer: M13 Forward Class: shotgun.
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Matches 213; Conservative
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AQ990346/c
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                                                                                                                                                                                  FEATURES
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nammalia; burneria; scuiroghachi; murldae; musinae; manalia; burneria; scuiroghachi; murldae; musinae; sokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Niyosawa, H., Yadi, K., Tomato, Y., Burda, H., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schrimh, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.M., Bradt, D. Prusic, V., Batalov, S., Beisel, K.W., Malake, J., Bradt, D. Prusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C. F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedaierski, R.M., King, B.L., Konagaya, A., Kucochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Percosky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Rempile, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Tasadale, R.D., Tomita, M., Verardo, R., Wagner, L., Wanshaw-Boris, A., Yanagisawa, M., Yang, I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 TATACTAAGTTGGCATTATAAAAAGCATTGC-TTATCAATTTGTTGCAACGAACAGGTC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733 AGTINATICATAGIG-CIGCATAIGIIGIGITINACAGIAIIAIGIAGICIGIITITIAAI 675
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
mapping to E. 2000, Nucleic
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/strain="W14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 South Building, Bath BA2 7AY,
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Photorhabdus luminescens
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Class: shotgun.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2011) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayaratu, N., Hiozane-Kishikawa, T., Komo, H., Nakamra, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
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                                                                                                                                               Rogers, J., Birney, E. and Hayashızakı, r.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 TCTGTCACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 167
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NIZIAN, Akimura, T., Arakawa, T.,

Alzawa, K., Akimura, T., Arakawa, T.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Miyazaki, A., Murata, M., Sasaki, D., Sadco, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/clone="L43040c03"
/tissue_type="whole body"
/dev_stage="18 days embryo"
/clone lib="RIKEN full-length enriched, 18 days embryo
whole body"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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.larity 97.9%; Pred. No. 2e-2
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AQ990861
REC01698 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01698, genomic survey
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/dev_stage="primary phase variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: ffrench-Constant RH Department of Biology and Biochemistry University of Bath
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0; Mismatches
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RESULT 11

AUTHORS REFERENCE

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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

(bases 1 to 770)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
20378633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res. Seg primer: M13 Reverse Class: shotgun.
AQ991774 170 bp DNA linear GSS 14-AUG-20
Rfc02039F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02039F, genomic survey
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Rfc02368F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02368F, genomic survey
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/clone="PLG02039F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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1. 770
/organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: ffrench-Constant RH
Department of Balology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
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                                                                                                                                                                           Photorhabdus luminescens
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Daborn,P.J., Bowen,D. and Blattner,F.R.
Agnomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 TIGATATITATATCATTITACGITTCTCGTICAGCTITITATACTAAGTIGGCATTATA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AAAAAGCATTGCTTATCAA-TTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Fax: (44) 1225 826779
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                              AQ990173 746 bp DNA linear GSS 14-AUG-2
Rfc00898 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00898, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
library"
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1 (bases 1 to 746)
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/strain="W14"
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clone="PLG00898"
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Location/Qualifiers
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Photorhabdus luminescens
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AQ991774/c
                                                                     AQ990173/c
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VERSION
KEYWORDS
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Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/clone="PLG01894"
                                                                       Department of Biology and Bioch
University of Bath
South Building, Bath BA2 7AY, U
Fax: (44) 1225 82621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
                                                           Contact: ffrench-Constant
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Photorhabdus luminescens
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Seq primer: M13 Forward
Class: shotgun.
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KEYWORDS
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                                                                       ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
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                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01894, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2%; Score 160.8; DB 28; Length 98.8%; Pred. No. 6.4e-21; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Photorhabdus luminescens"
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                                                                                                                                                                                                        Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
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clone="PLG02368F"
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 Photorhabdus luminescens
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AQ991039/c
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GSS 14-AUG-2000
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Rfc02270 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02270, genomic survey
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/clone_lib="photorhabdus luminescens strain W14 M13
library"
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1. .695
/organism="Photorhabdus luminescens"
/mol type="genomic DNA"
/strain="M14"
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Biochemistry
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Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Mucleic Acids Res.

Acids Res.

Seq primer: MI3 Forward
Class: shotgun.

L. 719

/ Organism="Photorhabdus luminescens"
/ mol type="genomic DNA"
/ strain="W14"
/ dev_stage="primary phase variant"
/ clone="PLG002270"
/ dev_stage="primary phase variant"
/ clone="PLG002270"
/ dev_stage="primary phase variant"
/ clone="PLG002270"
/ dev_stage="primary phase variant"
/ clone="Photorhabdus luminescens strain W14 MI3
| library"
/ note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into MI3 Janus."
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65.4%; Score 159; DB 28; Length 719;
Best Local Similarity 97.3%; Pred. No. 1.4e-20;
Matches 181; Conservative 0; Mismatches 3; Indels ;
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Search completed: September 9, 2004, 21:18:23 Job time : 1964.91 secs

238 GATTIC 243 |||||| 540 GATTIC 535

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Sequence 8, Applisequence 72, Applisequence 57, Applisequence 57, Applisequence 57, Applisequence 2, Applisequence 8, Applisequence 3, Applisequence 3, Applisequence 20, Applisequence 21, Appl
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                                                                                                                                                                              9, 2004, 19:34:38; Search time 306.981 Seconds (without alignments) 3982.858 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US09_NEW PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-695-14

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US-10-161-403-72

US-09-245-277-57

US-10-792-481-57

US-10-792-481-57

US-10-170-168-8

US-10-270-176-3

US-10-270-176-3
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ALIGNMENTS

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                                                                                        APPLICANT: Suttie, Janet Louise
APPLICANT: Suttie, Mary-Dell
APPLICANT: Que, Olideng Anic
APPLICANT: de Framond, Anic
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 700050SPS
CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn version 3.2
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                    Sequence 173, Application US/10403232
Publication No. US20030226164A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Bacteriophage lambda
US-10-403-232-173
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LENGTH: 243
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Pred. No. 1.1e-40;
O; Mismatches 0;
                                                        Ouery Match 100.0%; Score 243; DB 17; Best Local Similarity 100.0%; Pred. No. 1e-40; Matches 243; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 243; Conservative
OTHER INFORMATION: primer
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US-10-161-403-72
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US-10-161-403-72
      ; OTHEK INFORM
US-10-627-711-8
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Sequence 8, Application US/10627711
Sequence 8, Application OS/10627711
Sequence 8, Application No. US20040115812A1
Sequence 8, Application No. US20040115812A1
SEDENTALION OF TOWNEY ON THE TOWNEY OF TOWNEY FILE REPRENCE: 51236US
CURRENT APPLICATION NUMBER: US/10/627,711
CURRENT PILING DATE: 2003-07-28
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
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US-10-695-14
Sequence 14, Application US/10310695
Sequence 14, Application US/10310695
Fublication No. US20040110293A1
GENERAL INFORMATION:
APPLICANT: BNENKEL, BARBARA
TILE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REFERRANCE: DEBE:04908
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Bacteriophage lambda
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SEQ ID NO 8
LENGTH: 248
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Best Local Similarity 100.0
Matches 243; Conservative
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ORGANISM: Artificial
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LENGTH: 243
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135 TAICATITIACGITICTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 194
                                   GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 240
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APPLICANT: Lanahan, Anthony
APPLICANT: Lanahan, Anthony
APPLICANT: General Bernard
APPLICANT: General Holger
APPLICANT: Runer, Rohini
APPLICANT: Runer, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Chini
APPLICANT: Chini
APPLICANT: Mikolich, Raroly
APPLICANT: Mikolich, Bugene
TITLE OF INVENTION: IMPEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMPERER, CO/0744,805
CURRENT APPLICATION NUMBER: US/09/244,805
CURRENT APPLICATION NUMBER: 60/074,518
BARLIER FILING DATE: 1998-02-12
BARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARER: RastSEQ for Windows Version 4.0
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                                                                                                                                                                                                      US-09-244-805-57/c; Sequence 57, Application US/09244805; Publication No. US20030203840A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | LOCATION: (1) - (1763)
| OTHER INFORMATION: Y = C or T
| OTHER INFORMATION: n = A,T,C or G
| US-09-244-805-57
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Best Local Similarity 100.
Matches 243; Conservative
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ORGANISM: Eukaryote
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RESULT 6 US-09-245-277-57/c

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                    Publication No. US20030211984A1
GENERAL INFORMATION:
APPLICANT: Worley, Paul F.
APPLICANT: Lanahan, Anthony
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
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APPLICANT: Morley, Paul F.
APPLICANT: Lanahan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Kuner, Robini
APPLICANT: Kuner, Robini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Zhvovski, Eugene
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
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Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0;
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/245,277
CURRENT APPLICATION NUMBER: US/09/245,277
CURRENT FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/074,518
PRIOR FILING DATE: 1998-02-12
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 1763
TYPE: DNA
ORGANISM: Eukaryote
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FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/792,481
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/99/244,805
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/074,518
Sequence 57, Application US/09245277
Publication No. US20030211984A1
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OTHER INFORMATION: y = C or T

OTHER INFORMATION: n = A,T,C or G
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Publication No. US20040152658A1
GENERAL INFORMATION:
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US-10-270-176-8
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US-10-310-695-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Perkins, Edward
APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Ieung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLAFFORMS
FILE REPERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
FRIOR APPLICATION NUMBER: 60/294,758
FRIOR APPLICATION NUMBER: 60/294,758
FRIOR FILING DATE: 2002-05-30
FRIOR FILING DATE: 2002-03-30
FRIOR FILING DATE: 2002-03-31
FRIOR APPLICATION NUMBER: 60/366,891
FRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
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PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: 60/074,135
PRIOR FILING DATE: 1998-02-06
NUMBER OF ERQ ID NOS: 62
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 57-
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                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: (1)...(1763)
OTHER INFORMATION: y = C or T
COTHER INFORMATION: n = A,T,C or G
US-10-792-481-57
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FEATURE:
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US-10-161-403-113
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Publication No. US20040110293A1
GENERAL INFORMATION:
APPLICANT: BETER
APPLICANT: ENENEEL, BATER
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN BUKARYOTIC CELLS
FILE REPERBNCE: DEBE:019US
CURRENT APPLICATION UNDER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOPTHWARE: Patentin Ver. 2.1
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98.8%; Pred. No. 1e-39;
tive 0; Mismatches 3;
Pred. No. 2.6e-40;
; Mismatches 0;
    Best Local Similarity 100.0%; P. Matches 243; Conservative 0;
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Best Local Similarity 98.8
Matches 240; Conservative
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Query Match
Best Local Similarity 99.2'
Matches 243; Conservative
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LENGTH: 3695
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                                             APPLICANT: Wanner,
APPLICANT: Wanner,
APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLEASMIDS, STRAINS, AND METHODS OF USE
FILE REPERENCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/378,642
PRIOR APPLICATION NUMBER: 60/378,659
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 2959
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APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMINS, STRAINS, AND METHODS OF USE
FILE REFERENCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT APPLICATION NUMBER: 05/328,642
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
Sequence 8, Application US/10270176
Publication No. US20040033608A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10270176 Publication No. US20040033608A1 GENERAL INFORMATION:
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US-10-270-176-8
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               Publication No. US20040033608A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 243; Conserv
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(Sequence 13, Application US/10270176

Sequence 13, Application US/10270176

Publication No. US20040033608A1

GENERAL INFORMATION:

APPLICANT: Wanner, Barry

APPLICANT: Haldmann, Andreas

ITILE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE

FILE REFERENCE: 290.00140101.

CURRENT FILIAG DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 60/328,642

PRIOR APPLICATION NUMBER: 60/328,642

PRIOR PLING DATE: 2001-10-10

PRIOR PLING DATE: 2001-10-10

PRIOR PLING DATE: 2002-04-24

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTIN VELSION 3.0
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Score 231; DB 13;
Pred. No. 7.1e-38;
0; Mismatches 0;
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95.1%; Score 231; DB 13;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0;
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95.1%;
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4088 TATATCATTTTACGTTTCTCGTTCACCTTTTTATACTAAGTTGGGATTATAAAAAAAGCA 4147
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Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2;
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APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR FILING DATE: 2001-10-10
PRIOR PRILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 40
LENGTH: 5706
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                                                                      Score 231; DB 13;
Pred. No. 8.1e-38;
0; Mismatches 0;
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          ; OTHER INFORMATION: CRIM plasmid US-10-270-176-41
                                                                            95.1%;
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Best Local Similarity
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                                                                                                                                              APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REPRENCE: 290, 00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT APPLICATION NUMBER: 60/338,642
PRIOR APPLICATION NUMBER: 60/338,642
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 20
LENGTH: 4782
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APPLICANT: Haldiaman, Andreas
APPLICANT: Haldiaman, Andreas
APPLICANTON: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REFERENCE: 290.0014010.1
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR PLING DATE: 2001-0-10
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR FILING DATE: 2002-04-24
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99.2%; Pred. No. 7.7e-38;
tive 0; Mismatches 0;
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                                                                                     ; Sequence 20, Application US/10270176; Publication No. US20040033608A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: CRIM plasmid US-10-270-176-20
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 99.2
Matches 243; Conservative
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ORGANISM: artificial
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LENGTH: 5646
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US-10-270-176-41
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239 ATTTC 243 |||||| 4208 ATTTC 4212

Search completed: September 10, 2004, 00:14:07 Job time : 307.981 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on: September 9, 2004, 15:48:15; Search time 704.078 Seconds (without alignments) Title: (Without alignments) Forfect score: US-10-082-772B-3 Sequence: 102 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: 6940544 Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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em_htg_rod:* em_sy:* em_htgo_hum:* em_htgo_mus:* em_htg_vrt:*

Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

1 Droege,P. Sequence-specific dna recombination in eukaryotic cells Patent: WO 0116345-A 3 08-MAR-2001;

REFERENCE AUTHORS TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES			
Result No.	Score	* Query Match	Length	DB	ID		Desc	cription
	102	100.0	102	90	AX092114	 	AXO	92114 Sequ
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12	102		3484		A91914		A91	A91914 Sequence 1
13	102		3484		AR309120		AR3	09120 Sequence
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ນ 18 ຄະເ	102		5349		A71437		A71	A71437 Sequence 7
101	102		5349	ی ه	AKZU/455 BD069511		ARZ	0/455 Sequence 69511 Improved
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VERSION		92114.1	GI:134	1443	57			
REIWORDS SOURCE ORGANISM		Escherichia coli Escherichia coli	a coli					
		teria;	Proteobact	acte	eria, Gammapro	Gammaproteobacteria;		Enterobacteriales;
a-Madada d		erobact	erlaceae	ΣI	scherichia.			

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ORIGIN

FEATURES

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Mammalia; Eutheria; Primates; Cararhini; Hominidae; Homo.

(bases 1 to 1090)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, B.R. NotI flanking sequences: a tool for gene discovery and verification of the human genome
Nucleic Acids Res. 30 (14), 3163-3170 (2002)
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Mallic,B.; Hirono,J.; Sato,T. and Buck,L.B.
Combinatorial receptor codes for odors
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
Direct Submission
Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
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Homo sapiens genomic sequence surrounding NotI site, clone
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Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
Direct Submission
Submitted (20-JAN-1999) Neurobiology, Harvard
Longwood Avenue, Boston, MA 02115, USA
3 (bases 1 to 1421)
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Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 102; Conservative 0; Mismatches 0;
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/clone="NB1-850S"
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Zabarovsky, E.R.
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Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,

(Dases 1 to 979)

Sadoulet-Puccio, H.M., Feener, C.A., Schaid, D.J., Thibodeau, S.N.,

Michels, V.V. and Kunkel, L.M.

The genomic organization of human dystrobrevin

Neurogenetics 1 (1), 37-42 (1997)
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Sadoulet-Puccio,H.M., Feener,C.A. and Kunkel,L.M.
Direct Submission
Submitted (09-JAN-1997) Genetics, HHMI, 320 Longwood Avenue,
Boston, MA 02115, USA
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U84530
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450. .530
/gene="DTN"
/number=2
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Matches 102; Conservative
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Matches 102; Conservative
        Peter (DE)
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ACCESSION VERSION KEYWORDS SEGMENT DEFINITION

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YTELEDQHVWTAIPFCSMYILALVGNGTILYIITDRALHEPMYLFLCLLSITDLVLC
YTELEMAPPREVALLAMAFPREYALLAMAFPRYATCHTH
TSILMAWVIGKIGLAVTRGLLFVFPVILIERLPFCGHHIIPHTYCEHMGIAKLACA
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Sequence update by submitter
On Dec 7, 1999 this sequence version replaced gi:4680261.
Location/Qualifiers
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/note="G-protein-coupled receptor"
                                                                                                                             'product="odorant receptor S19"
                                                                                                                                                                                      /product="odorant receptor S19"
/protein_id="AAD27596.2"
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Selsted,M.E. and Ouellette,A.J.
Antibiotic cryptdin peptides and met
Patent: US 5840499-A 69 24-NOV-1998
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/mol_type="genomic DNA"
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                                                                                                   /db_xref="taxon:10090"
<291. .>1310
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Antibiotic cryptdin peptides and methods of their use Patent: Location/Qualifiers
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Selsted,M.B. and Ouellette,A.J.
Antibiotic cryptdin peptides and methods of their use
Patent: US 5731149-A 69 24-MAR-1998;
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Sequence 69 from patent US 6300470.
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/organism="unknown"
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                                                                                                                                                    Query Match 100.0%; Score 102; DB 6; Length 2408; Best Local Similarity 100.0%; Pred. No. 9.4e-15; Matches 102; Conservative 0; Mismatches 0; Indels 0
     1 (bases 1 to 2408)
Selsted, M.E. and Ouellette, A.J.
Antibiotic cryptdin peptides and methods of their use
Patent: US 6300470-A 69 09-OCT-2001;
Location/Qualifiers
1..2408
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                                                                                                                                                                                                                                                                                    468 AACAGGTCACTATCAGTCAAAATAAATCATTATTTGATTTC 509
                                                                                                                                                                                                                                                                     61 AACAGGICACTAICAGICAAAAIAAAAICAIIAIIIGAIIIC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 102; DB 6;
100.0%; Pred. No. 9e-15;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue-specific promoters from sugar beet Patent: EP 1207204-A 4 22-MAY-2002; KWS Saat AG (DE)
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                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .3049 Beta vulgaris"
/organism="Beta vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:161934"
1. .2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3049 bp
Sequence 4 from Patent W00240687.
AX449167.1 GI:21697968
                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 from Patent EP1207204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hehl, R., Kloos, D. and Stahl, D.J.
                                                                                                             /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                               /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                 AX430197.1 GI:21655562
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Best Local Similarity 100.
Matches 102; Conservative
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Beta vulgaris
Unclassified
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TATA_signal
mRNA_
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JOURNAL
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SOURCE
             REFERENCE
AUTHORS
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AX430197
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de Hostos, E.L.
Direct Submission
Submitted (II-APR-1990) De Hostos E.L., Max-Planck-Institude for Submission
Submitted (II-APR-1990) De Hostos E.L., Max-Planck-Institude for Biochemistry, Am Klopferspitz 18A, 8033 Martinsried, FRG
The sequence is a composite of a cDNA (for CDS region) and genomic. See <X16179> for intron between bases 717-718.
See <X16180> for bases 61-3104.
Location/Qualifiers
1...3111
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 481 to 3111)
de Hostos, E.L., Schilling, J. and Grossman, A.R.
Structure and expression of the gene encoding the periplasmic arylsulfatase of Chlamydomonas reinhardtii
Mol. Gen. Genet. 218 (2), 229-239 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           скекмыs all bp mRNA linear
Chlamydomonas mRNA for periplasmic arylsulfatase.
X52304
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/mol_type="mRNA"
/strain="CW15."
/db_xref="taxon:3055"
/clone_lib="Lambda gtll (cDNA) and EMI
481. .566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site"
                                                                                                                                                                                                      location/Qualifiers
1.3049
/organism="Beta vulgaris"
/mol type="unassigned DNA"
/db_xxef="taxon:161934"
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/note="transcription start
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/note="inverted repeat A'"
616. .2556
                                                                                                                                       Tissue specific promoters
Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="inverted repeat A"
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                                                                                                                Hehl, R., Kloos, D. and Stahl, D.J.
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2877. .2883
2928. .3049
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0

Indels

Length 3484;

09

PAT 12-JUN-2003

linear

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420 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTIGTTGCAACG 479
                                                                                           1 CIGCTITITIATACTAAGTIGGCATTATAAAAAAGCATIGCTTATCAATTIGTIGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 3484)
Funaba,Y., Koike,J., Tanahashi,M., Okazaki,S. and Ito,M.
Remedies for intramedullary diseases
Patent: US 6555529-A 1 29-APR-2003;
                                                                                                                                                                             61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                        180 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC
                 ; Score 102; DB 6;
; Pred. No. 8.8e-15;
0; Mismatches 0;
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Sequence 1 from patent US 6555529.
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Sequence 1 from patent US 6395963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                   AR309120.1 GI:31700962
              Query Match
Best Local Similarity 100.0%;
Matches 102; Conservative 0
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          Query Match
Best Local Similarity
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AR309120
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AR372694
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SOURCE
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                                                                                                                                      / LTAINS LAKY IRYPGVEAAVASVAHAADTKKENEVVI FUDDQDAIQNST
HPHYMPSLHKY IRYPGVELSQYFVTTPVCCPSRTNLCAASSPTTPTSPACCLEPTVAGP
SRAMMASTSPTCRCGSRTKALTPTTAKASSLWTTPSATTSRCRGLGRYRCPVTPYTFDY
NTRLORNGATPNI YPGEYSTDVI INDKGVAQI KSAVAAGKPFYAQI SPI ABPHTSTDIST
NPATGVTRSYFPPP IPARPHWOLFSDANLPGGSQOEPLRGGRERQARLDPRPAGFAE
QPHLPGGDLPPAPEWAGPVELI EQVVKTLDEAGVLDNTY I I YSADNGYHVGAHRFGA
GKTTGYBEDLRVPFLLRGPGI KASKSDKPQNSKVGLHVDFAPTI LGLAGASHLLGDKC
                                                                                                                                                                                                                                                                                   LDGTPLGLYANDDGTLPSDYPREEDHRQQFQSEFWGGMSDELLQNLRSQPNATWKVVR
TYDESSKQGMKLIAQCTNRRELYDLRKDPRGELVNIXDKAKFAVRSRLEGLLAVLAVCK
GESCSNPWKILIAPDGTVKNFTQALNSKYDRIYNATRPFTYKRCLPYLDWDNEDSQFKT
QIRGANPAAGVGHHLIAAASERAIATRRRAQAAVSAELADGPAVFQAKVEEKSVPVP
QDILKADVEKWPAFNNAEYYLAA
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note="unnamed protein product; protein precursor (AA -21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Uaridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 3484)
Ohl, S.A. and Klab, J.
NEMATOBE-INDUCIBLE REGULATORY DNA SEQUENCES
Patent: WO 9822599-A I 28-MAY-1998;
LEE FREDERIQUE MARIANNE V D (NL); OHL STEPHAN ANDREAS (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
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100.0%; Pred. No. 9e-15;
ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
                                                                                                                                                                                                                                                                                                                                                                                                               note≈"signal peptide (AA -21 to -1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                679. .2553
/product="mature protein (AA 1-625)"
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/note="unnamed protein product"
/codon start=2
                                                                                                                         xref="SWISS-PROT:P14217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
/strain="C24"
                                                             /proteIn_id="CAA36545.1"
/db_xref="GI:18174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB69451.1"
/db_xref="G1:6740782"
/translation="M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A91914 3484 bp Sequence 1 from Patent W09822599.
                                                                                                    'db_xref="GOA:P14217"
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DEFINITION

RESULT 12

A91914 LOCUS

ACCESSION VERSION

KEYWORDS

Matches

g à P_D

ORIGIN

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

ORIGIN

Length 3484;

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                                                                     420 CTGCTTTTTTTTATACTAAGTTGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                  1 CIGCITITITATACTAAGTIGGCATTATAAAAAGCATIGCTIATCAATTIGTIGCAACG
    Gaps
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Ohl,S.A., Sijmons,P.C., Klein-Van der Lee,F.M., Goddijn,O. and
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                                                                                                                                                 480 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klap,J.
Nematode-inducible regulatory DNA sequences
Patent: US 6395963-A 1 28-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 102, DB 6; Best Local Similarity 100.0%; Pred. No. 8.8e-15; Matches 102; Conservative 0; Mismatches 0;
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                                                                                                       PAT 31-JAN-2002
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420 CIGCITITITATACIAAGITGGCATTATAAAAAGCATIGCTTAICAAITIGTIGCAACG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 3484
Corganism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Location/Qualifiers
                                                                                                       BD007602 3484 bp DNA Nematoda-induced regulatory DNA sequence. BD007602
                                                                                                                                                       JP 2001503992-A/1.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                           BD007602.1 GI:18635975
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Best Local Similarity 100.
Matches 102; Conservative
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                                                                                    RESULT 15
BD007602
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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480

Search completed: September 9, 2004, 19:34:31 Job time : 706.078 secs Н

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

9, 2004, 13:30:05 ; Search time 116.156 Seconds (without alignments) 3730.479 Million cell updates/sec September Run on:

US-10-082-772B-3

Perfect score:

1 ctgcttttttatactaagtt......taaaatcattatttgatttc 102 IDENTITY NUC Scoring table: Sequence:

3373863 seqs, 2124099041 residues Searched:

Gapop 10.0 , Gapext 1.0

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Match 100% Post-processing: Minimum Match 0% Maximum Match 100

N_Geneseq_29Jan04:* Database

geneseqn2003as:*geneseqn2003bs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003cs:* geneseqn1990s:* geneseqn1980s:* geneseqn2000s:* geneseqn2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

	Description	Aaf61419 E. coli a	Rat		Aav34987 Arabidops	Aav44332 Murine mM	Aav42708 Mouse mas	Aav23239 T-DNA of	Aav23242 Plasmid p		Aaf61418 Bacterion		Acc44676 Murine rD				Acc83020 Bacterion	Aaz30709 Rat neuro	Acc44716 Plasmid p	Abt16615 Artificia	Aat18924 Plasmid p	Aaf30800 Vector pl	Vector	Vector
SUMMAKIES	ID	AAF61419	AAT30737	ABN81284	AAV34987	AAV44332	AAV42708	AAV23239	AAV23242	AAQ50319	AAF61418	ACC85316	ACC44676	ABT16636	AAF79770	ABQ80306	ACC83020	AAZ30709	ACC44716	ABT16615	AAT18924	AAF30800	AAF30801	AAF30798
	Query Match Length DB	102 4	2408 2	3049 6		3757 2		5349 2	5611 2		243 4	248 8	282 7	282 7	610 5	1469 7	1469 7	1763 2	4346 7	4346 7	4909 2	5641 4	5670 4	5826 4
÷	Query Match L	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4
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	AAI30/99 VECTOR DI	2 Aaq45682 Sequencir	1 Aaf61421 E. coli	3 Aal62713 Escherich	6 Aac55386 Recombina	9 Acc59569 Nucleic a	Aac55422	7 Aac55437	4 Abz58764 Entry vec	5 Aac55425 Entry vec	l Aac55431 1	Aac55434	B Aac55428 Entry vec	Aac55446 Entry	Aac55443	Aac55449]	Aac55440	Aac55452 Entry	Adc06860	Adc06864	Abk88866	
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9	40.	98.4	96.9	96.5	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	90.4	90.4	90.4	
7	# · OO T	100.4	98.8	98.4	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	92.2	92.2	92.2	0
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ALIGNMENTS

AAF61419 standard; DNA; 102 (first entry) 05-JUN-2001 AAF61419; RESULT 1 AAF61419

BP

Sequence-specific recombination, SSR, integrase, gene therapy; somatic; targeted integration; attL, ds. E. coli attL DNA fragment.

Escherichia coli.

DE19941186-A1. 01-MAR-2001. 99DE-01041186. 30-AUG-1999;

(DROE/) DROEGE

99DE-01041186.

30-AUG-1999;

Droege P;

WPI; 2001-246016/26.

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.

Claim 3; Page 14; 24pp; German.

This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences

Gaps

0;

Indels

Length 2408;

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408 cigcirriranaciragriggcarraraaaaagcarrgcrrarcaarrigrigcaacg 467
                                                                            CTGCTTTTTTATACTAGCTTGCCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                 Beet; promoter; carbohydrate metabolism; invertase inhibitor; fructosyl transferase; levan sucrase; nitrogen transporter protein; pathogen resistance; plant; transgenic; ds.
    Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;
                                                                                                                                                  468 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC
                                                                                                                         61 AACAGGICACIAICAGICAAAAIAAAAICAITAITIGAIIIC
                            100.0%; Score 102; DB 2;
100.0%; Pred. No. 6.5e-19;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             Beet promoter polynucleotide SEQ ID NO 4.
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                                 100.0%; Fr.
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2928. /*tr
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/*tag= h
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                                                                                                                                                                                                                                                       (first entry)
                                                       Conservative
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                                        Local Similarity
nes 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                   Beta vulgaris
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                                                                                                                                                                                                                                                       22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                             TATA_signal
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                                                                                                                                                                                                                                  ABN81284;
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                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                 Query Match
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                                                                                                                                                                                                ABN81284
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                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity against a broad range of incestinal and opportunistic pathogens. Rat cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2 gene, or corresponding cDNA (see also T30734), can be used to produce large amounts of cryptdin-2 for use in treating inflammatory pathologies of the intestine
                                                                   09
                                                                                CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cryptdin peptide(s) - which have antimicrobial activity, in the detection and treatment of inflammatory pathologies.
                                                                                                                                                                                                                                                                                                                                                                                                 codon start= 1174. .1176
'note="exon 1 codes for the 5' untranslated region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "exon 2 codes for cryptdin-2 and 3' untranslated
                                                                   1 CTGCTTTTTTTTTTATAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                             Gaps
                                                                                                                                                                                                                                                                                        Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation; antiinflammatory; inflammatory bowel disease; pancreatitis; cancer; tumour; ileitis; ds.
                                             ·,
                    Length 102;
                                            Indels
                                                                                                                               61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTG 102
                                                                                                                61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
Sequence 102 BP; 35 A; 16 C; 13 G; 38 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHRINER'S HOSPITAL FOR CRIPPLED CHILDREN.
                                              ..
                    Score 102; DB 4;
Pred. No. 4.5e-19;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         cryptdin-1 prepro sequence" 1345. .1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 31; Page 64~65; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                 AAT30737 standard; DNA; 2408 BP
                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US013328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00342268
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P-PSDB; AAR98787, AAR98792.
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                                              102; Conservative
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                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                    Rat cryptdin 2 gene.
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9616075-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used partic.
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The invention relates to a promoter (A) that is: (i) any of the sequences ABN81281-ABN81284; (ii) the complement of (i); or (iii) a sequence that hybridises to (ii). (A) are used, specifically in Beta vulgaris, to control expression of transgenes, particularly to alter carbohydrate metabolism; reduce loss of storage substances; express invertage inhibitor, fructosyl transferase, levan sucrase or genes that encode transporter proteins for nitrogen compounds, or increase resistance to, or tolerance of, pathogens. (A) provide tissue-specific transgene expression, either in roots or above-ground parts, so avoid pleiotropic effects, e.g. when expressing invertage inhibitor
                                                                                                                                                                                                             New tissue-specific promoters from Beta vulgaris, useful e.g. for altering carbohydrate metabolism, express transgenes selectively in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 30-31; 57pp; German.
     DJ;
Stahl
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This DNA fragment obtainable from Arabidopsis thaliana is capable of promoting rook knot and cyst nematode-inducible transcription of an promoteries associated DNA sequence when reintroduced into a plant. The promoteriess GUS construct binary vector pWGG553 was mobilised by triparental mating to Agrobacterium tumefaciens MGG101 and the resulting strain was used for Arabidopsis root transformation. Line pMGG553455 was identified as a line which showed strong GUS expression inside syncytia and giant cells induced by the cyst nematode Heterodera schachtii and the root knot commenced Meloidogyne incognita, respectively. Promoter tags from line pMG553425 were sequenced. The claimed DNA fragment is nematode feeding site-specific. Also claimed are: (1) a portion or variant of the above creapable of promoting root knot and cyst nematode inducible transcription of an associated DNA sequence when reintroduced into a control, and which causes the production of a plant cell-disruptional control, and which causes the production of a plant cell-disruptional control, and which causes the production of a plant cell-disruption control, and which causes the production of a plant cell-disruption control, and which causes the production of a plant cell-disruption control, and which causes the production of a plant cell-disruption control, and which causes the production of a plant cell-disruption control, and which causes the production control cell-disruption control control, and which causes the production control cell-disruption control control control control control control control control control cell-disruption control cell-disruption control cell-disruption control cell-disruption control cell-disruption control cell-disruption cell-disruption control cell-disruption control cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disruption cell-disrupt
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                                                       o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Arabidopsis thaliana DNA promoter - useful for, e.g. generating plant reduced susceptibility to plant parasitic nematodes.
                                                                                                         09
                                                                                                       CTGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promoter; nematode feeding site; root knot nematode; cyst nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meloidogyne incognita; Heterodera schachtii; Globodera pallida;
transgenic plant; pest resistance; crop protection; ds.
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0
     Length 3049;
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                                                       Indels
                                                                                                                                                                                                                                                     2458 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis nematode feeding site-preferential promoter.
                                                                                                                                                                                                   61 AACAGGTCACTATCAGTCAAAAAAAAATCATTATTTGATTTC 102
Query Match 100.0%; Score 102; DB 6; Best Local Similarity 100.0%; Pred. No. 6.7e-19; Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start= 3482. .3484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 22-24; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana; ecotype C24.
                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                  AAV34987 standard; DNA; 3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-EP006472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Der Lee FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOGE-) MOGEN INT NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-312484/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1996;
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28-SEP-1998
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a plant cell having incorporated into its genome the chimeric DNA of (2); (6) a root system of a plant consisting of the cells of (5); (7) a plant consisting of the cells of (5); (7) a plant especially a potato plant; (8) a plant grafted onto the root system of (6); (9) a part of a plant, selected from seeds, flowers, tubers, roots, leaves, fruits, pollen and wood, obtained from the plant of (7) or (8), and (10) a crop consisting of the plants of (7) or (8). The DNA fragment can be used to identify subfragments capable of promoting transcription of an associated DNA sequence in a plant. It can also be used for making hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be used for transforming plants (all claimed). The DNA sequence can be used to reduce the susceptibility of a plant to parasitic nematodes. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                             CTGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCP-6 zymogen; mouse; mast cell protease 6; mMCP-7; tryptase-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy; ss.
                                                                                                                                                                                                                                                 Query Match 100.0%; Score 102; DB 2; Length 3484; Best Local Similarity 100.0%; Pred. No. 6.8e-19; Matches 102; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                   Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      61 AACAGGICACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                         480 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 521
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'note= "contains introns"
1803. .1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV44332 standard; DNA; 3757 BP
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1873. .2011
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/*tag= d
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*tag= e
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2861. .2933
/*tag= i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine mMCP-6 zymogen gene.
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/number= 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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exon

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6). The invention provides sequences shown in AAW63160 to AAW65169 that are inhibitors of mMCP-6. These peptides which are tryptase-6 complex inhibitors, can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, uriticaria and anticedema, eczematous dermattis; (atopic dermattis), hyperproliferative skin disease, anaphylaxis, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory skin conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 CIGCITITITATACTAAGTIGGCATTATAAAAAGCATIGCTITATCAATTIGTIGCAACG 433
                                                                                                                                                                                                                     - used to treat mast cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCTTTTTTATACTAGGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barstar; barnase inhibitor; fertility restoration; male-sterile line;
                                                                                                                                                                                                                                                                                                                            This represents the cDNA sequence of the mouse mast cell protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "region coding for phosphinothricin acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing 3' untranslated end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 102; DB 2;
100.0%; Pred. No. 6.8e-19;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium T-DNA gene
                                                                                                                                                                                                                       Tryptase-6 complex inhibitory peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= RB
/note= "right boarder"
complement(98. .331)
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/*tag= d
                                                                                                                                                                                                                                                                                   Disclosure; Page 42-43; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                           inflammatory disorders e.g. asthma
                                                                                                (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1. .25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 102; Conservative 0
                 98WO-US001865
                                                         97US-0037090P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid pTTS24; T-DNA; ds
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                                                                                                                                          Stevens RL, Huang C;
                                                                                                                                                                                 WPI; 1998-437390/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-DNA of pTTS24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feature
                     30-JAN-1998;
                                                         05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV23239;
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misc
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This nucleotide sequence includes a coding region for mouse mast cell procease 6 (mMCP-6, see AAW64242). The invention provides: compositions comprising an isolated tryptase-7 (such as mMCP-7, see AAW64233); a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product; a nucleic acid encoding a serine procease (SP); and a method of producing a mature SP. Tryptase-7 polypeptides can be used for treating disorders mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        undesirable thrombus clot formation such as myocardial infarction and reocclusion following angioplasty of blood clots associated with pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma; tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria; antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis; hyperproliferative skin diseas; peptic ulcer; hyperresponsiveness; inflammatory skin condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                      New compositions containing tryptase-7, e.g. mouse mast cell protease-7 are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary thrombo-embolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse mast cell protease (mMCP-6) nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AACAGGTCACTATCAGTCAAAAAAAAAAAATAATTTGATTTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 102; DB 2;
; Pred. No. 6.8e-19;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vein and peripheral arterial thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 68-69; 92pp; English
                                                                                                                                                                                                                                               (BGHM ) BRIGHAM & WOMENS HOSPITAL.
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    2934. .3098
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Best Local Similarity
Matches 102; Conserv
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                                                                                   WO9824886-A1
                                                                                                                                                                  25-NOV-1997;
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                                                                                                                         11-JUN-1998
                                                                                                                                                                                                                                                                                        Stevens RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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AAV42708 RESULT

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/label= 3' nos
/label= 3' nos
/lace= "region containing 3' untranslated end of nopaline
synthase gene of Agrobacterium T-DA"
complement(318. .869)
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                                                                                                                                                                                                                                                                                                                                                                             /*tag= f
//label= 3'.chs
/note= "region containing 3' untranslated end of chalcone
synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the preparation of an improved Bacillus amyloliquefactions barstar, i.e. barnase inhibitor, which can be used to restore fertility to male-sterile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                          note= "promoter of TA29 gene of Nicotiana tabacum"
285. .2560
                                                                                                                                                /note= "region coding for phosphinothricin acetyl transferase"
                                                                                                                                                                                                                               Note= "35S promoter of Cauliflower Mosaic Virus"
740. .2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5611 BP; 1389 A; 1342 C; 1353 G; 1527 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 102; DB 2; Length 5611; 100.0%; Pred. No. 7.2e-19; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACAGGICACTATCAGICAAAATAAAATCATTATTTGATTTC 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                             product= "improved barstar
                                                                                                                                                                             complement (870. .1702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 45-48; 54pp; English.
 Location/Qualifiers
complement(39. .317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                               *tag= d
label= PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-EP004739.
                                                                                                                                                                                                   *tag= c
label= P35S
                                                                                                                                                                                                                                                                                                                                                            2561. .2892
                                                                                                                  '*tag= b
label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ50319 standard; DNA; 201
                                     /*tag= a
/label= 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams M;
                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3140
                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ50319
                                                                                                                                                                                  promoter
     Key
3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ50319
ID AAQ5
XX
AC AAQ5
                                                                                                 CDS
                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                              CDS
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     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4885 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 4826
                                                                                                                                                                          /label= 3'_chs
/note= "region containing 3' untranslated end of chalcone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amyloliquefacions barstar, i.e. barnase inhibitor, which can be used to restore fettility to malle-sterile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the preparation of an improved Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CIGCITITITALACTAAGITGGCATTATAAAAAAGCALTGCTTATCAAITTGLTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barstar; barnase inhibitor; fertility restoration; male-sterile line; plasmid pLH48; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
             note= "35S promoter of Cauliflower Mosaic Virus" 281. .3969
                                                                                (WO9213956)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4825 AACAGGICACTATCAGTCAAAATAAAATCATTAITTGATTTC 4784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGGICACTAICAGICAAAAIAAAAICAITAITIGAIIIC 102
                                                                                rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 102; DB 2;
100.0%; Pred. No. 7.1e-19;
tive 0; Mismatches 0;
                                                              label= PE1
note= "promoter of E1 gene of 970. .4245
                                                                                                                          product= "improved_barstar"
                                                                                                                                                                                                                                             '*tag= h
'note= "T-DNA left border"
                                                                                                                                                                                                                            complement (5325. .5349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 41-43; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase gene"
                                                                                                                                                                                                                                                                                                                                                         97WO~EP004739
                                                                                                                                             246. .4577
                                                                                               .4245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
label=
                                                                                                                *tag=
                                                                                                                                                               *tag≍
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                       01-SEP-1997;
                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                            WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1996;
                                                                                                                                                                                                                                                                                                                          12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michiels F,
                                 promoter
                                                                                              CDS
                                                                                                                                             CDS
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27-APR-1994

17-SEP-1993

for

Chip

probes

Synthetic.

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DNA in a enkaryotic cell, comprising introducing two DNA sequences (I, into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                            Sequence-specific recombination of DNA in eukaryotes, useful particulariy for somatic cell gene therapy, uses an integrase to effect recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCITITITIATACTAAGTIGGCATTATAAAAAAGCATIGCITATCAATTIGTIGCAACG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
                                                                                                                                                                                                        This invention describes a novel sequence-specific recombination (SSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vegetable plastid transformation; transgenic; recognition sequence; plant; site-specific integration; nutrition; seed production; chemical production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100.4; DB 4; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinase lambda integrase attP DNA recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACAGGICACTATCAGICAAAATAAAATCATTATTIGATTTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 35; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUNG-) SUNGENE GMBH & CO KGAA.
                                                                                                                                                               Claim 2; Page 13; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2001; 2001DE-01063159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.4%;
al Similarity 99.0%;
101; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-2002; 2002WO-EP014303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC85316 standard; DNA; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                         WPI; 2001-246016/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-541820/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                            between att sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003054201-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biesgen C;
Droege P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACC85316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC8531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAQ50309-26 are probes which were used on a chip for capturing a number of target polynucleotides. A group of these probes may be attached on cells which form part of a single chip. The oligonucleotides to be detected are labelled and are complementary to the set of capture probes used. The detection chip may be used to detect a number of different polynucleotides concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         or capturing polynucleotide - has several different complementary fixed on cells at different sites on single tip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100.4, DB 2; Length 201;
Pred. No. 1.3e-18;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAGGTCACTATCAGTCAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 144
                                                                                                      Probe; chip; cell; detection; label; capture probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage lambda attP DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99DE-01041186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DE-01041186
                                                                                                                                                                                                                                                                            92JP-00042829
                                                                                                                                                                                                                                                                                                                   92JP-00042829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                           (HITA ) HITACHI LTD
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-330600/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                 Detection probe 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DROE/) DROEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19941186-A1
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                                                                                                                                                                                         JP05236997-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1999;
                                                                                                                                                                                                                                                                            28-FEB-1992;
                                                                                                                                                                                                                                                                                                                   28-FEB-1992;
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Matches 101;

Query Match

61 103

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05-JUN-2001

AAF61418;

RESULT 10

AAF61418

01-MAR-2001

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genome. ACC44612

cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the

exemplification of the present invention

transgenic animal (e.g. a fish, insect, reptile, amphibian, arachmid, or mammal) by introducing (II) by cell fusion, lighd-mediated transfection by a carrier system, microinfection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic

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                                                                                                                                                                                                              147 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 206
derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. erzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification
                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site, integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system; gene, ds.
                                                                                                                                                                                    1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greene A, Leung J, Fleming
                                                                                                                                                            ;
                                                                                                                                  DB 8; Length 248;
                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                        207 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 248
                                                                                                        Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       61 AACAGGICACIAICAGICAAAAIAAAAICAIIATIIGAIIIC 102
                                                                                                                                               Pred. No. 1.4e-18;
                                                                                                                                                          0; Mismatches
                                                                                                                                  Score 100.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHRO-) CHROMOS MOLECULAR SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2001; 2001US-0294758P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0366891P
                                                                                                                                  98.48;
                                                                                                                                                                                                                                                                                                                                   ACC44676 standard; DNA; 282
                                                                                                                                              99.0%;
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                          Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perez C,
Shellard
                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200297059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ы́ ю́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perkins Stewart
                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus
                                                                                                                                                                                                                                                                                                                  ACC44676
                                                                                                                                                                                                                                                                                                                                            00000000X8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                                                                                                                                                                         156 CAGCTITITIATACTAAGTIGGCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, trNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and
                                                                                                                                                                                                                                                          1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant artificial chromosome, PAC, transgenic plant, vaccine,
blood factor, herbicide, stress, agronomical, nutrient quality,
bacterial artificial chromosome, BAC, yeast artificial chromosome, YAC,
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          0;
                                                                                                                                                                                         DB 7; Length 282;
                                                                                                                                                                               Score 100.4; DB 7; Lucar
Pred. No. 1.4e-18;
.....rrhes 1; Indels
                                                                                                                                                                                                                                                                                                                         AACAGGICACTATCAGTCAAAATAAAATCATTATTTGATTTC 257
                                                                                                                                                            Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 263-264; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perkins
                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2002; 2002WO-US017451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2001; 2001US-0294687P. 04-JUN-2001; 2001US-0296329P.
                                                                                                                                                                                           98.4%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT16636 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perez C, Fabijanski SF,
                                                                                                                                                                                                                             Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-140436/13.
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200296923-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABT16636;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHRO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AGRI-)
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                            ABT16636
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one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (1) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a

The present invention describes a eukaryotic chromosome (I) comprising

Example 2; Page 207; 272pp; English.

interest

Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of

WPI; 2003-140461/13.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attp) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibiotic resistance. The present sequence is the attP coding region
                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
biopharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trail in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (BAC). This polynucleotide sequence represents an oligo relating to the method for producing plant artificial chromosomes of the invention
                                                                                                                                                                                                                                                                                                                                 1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Attachment P region; attP; recombination; marker gene removal; ds.
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                         Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                         61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 257
                                                                                                                                                                                                               Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       DB 7;
                                                                                                                                                                                                                                                   Score 100.4; DB 7 Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda attachment P region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 3D; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF79770 standard; DNA; 610 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-00021937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2000; 2000WO-GB003543
                                                                                                                                                                                                                                                       98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                       101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-266072/27.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF79770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AAF79770
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The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 bp portion of lambda phage DNA contained in a plasmid. The amplified comprises at least one support having at least one oligomer and/or collymer applied on it. The printed material is useful in a method for synthesising DNA where the product of amplification and/or ligation is contained to the insertion/deletion, single nucleotide insertion/deletion, single nucleotide contained in a method for containation of nucleotide insertion/deletion, or SNP analysis.

CC determination of protein expression. The printed material is useful in cresearch applications, or from the printed materials seasily and immediately. From the copymers from the printed materials analyor polymer can be obtained immediately and directly, without need to make a request for it. The climpant and time while eliminating the need to make a request for it. The labour and time while eliminating the need to use special equipment or familities mhis while eliminating the need to use special equipment or familities mhis the printed material is a mick, efficient and
280 CAGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer
                                                                                                                                                                                                                                                                                                                                                                                           Primer, PCR; amplify, lambda phage; printer material; insertion; deletion; single nucleotide polymorphism; sequencing; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100.4; DB 7; Length 1469; Pred. No. 1.7e-18; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       printed material is a quick, efficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                     340 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 31-32; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   facilities. Thus, the printed mater
inexpensive sample delivery system
                                                                                                                                                                                                                                                                                                                                                    Lambda fragment in plasmid DNA.
                                                                                                                                                                                                                ABQ80306 standard; DNA; 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2002; 2002WO-JP009766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2001; 2001JP-00291249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.4%;
Best Local Similarity 99.0%;
Matches 101; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DNAF-) DNAFORM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003027991-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      applied on it.
                                                                                                                                                                                                                                                                                                        27-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                            ABQ80306;
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                                                                                                                                                                      RESULT 15
ABQ80306
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0;

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Indels

98.4%; Score 100.4; DB 5; Length 610; llarity 99.0%; Pred. No. 1.5e-18; Conservative 0; Mismatches 1; Indels 0

Best Local Similarity
Matches 101; Conserv

Query Match

OY 1 CTGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGTATATAAAAAAGCATTGTAATGAA
Db 949 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGTTTTCAA
OY 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
Db 1009 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 1050
Search completed: September 9, 2004, 18:05:40
JOb time: 117.156 secs

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Fri Sep 10 09:49:25 2004
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Query Match
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Sequence 10, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 78, Appl
Sequence 4, Appli
Sequence 1, Appli
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69, Appl
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13, Appli
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 50, Appl
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Sequence 24, Appl
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                                                                             9, 2004, 17:33:11; Search time 22.4903 Seconds (without alignments) 2516.866 Million cell updates/sec
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Sequence 69, P
Sequence 69, P
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                                                                                                                                                   1 ctgcttttttatactaagtt.......taaaatcattatttgatttc 102
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

? /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

/ cgn2_6/ptodata/2/ina/6A_COMB.seq:*

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? /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*

? /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-728-785A-18
US-08-56-978B-78
US-09-630-929-4
US-09-630-98A-1
US-09-107-532A-667
US-09-453-702B-50
US-09-453-702B-66
US-09-453-702B-66
US-09-451-708-24
US-09-91-389-3
US-08-956-171E-269
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US-08-482-279-69
US-08-342-268-69
US-09-3015-968-69
US-09-30-386-69
US-09-380-090A-1
US-09-380-090A-1
US-09-068-101-7
US-09-068-101-7
US-09-068-101-10
US-09-068-101-10
US-08-021-667A-18
US-08-021-667A-18
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            682709 seqs, 277475446 residues
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APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods TITLE OF INVENTION: Of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Rhoppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
                                  PCT-US93-04384-1

US-08-308-872B-1

US-08-316-246-1

US-09-134-001C-2801

US-09-621-976-14383

US-09-29-849B-25

US-09-38B-92-25

US-08-142-368B-25

US-08-967-727-25

US-08-967-727-25

US-08-967-727-25

US-08-967-727-25

US-08-967-727-25

US-08-967-727-25

US-09-312-464-25

US-09-312-464-25

US-09-312-464-25
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           US-09-854-799-21
PCT-US91-08525-21
                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-NAX-1992
ATTORNEY/AGENT: 11 PROPRATION:
                                                                                                                                                                                                                                                                                                                                            ; Sequence 69, Application US/08486013; Patent No. 5731149; GENERAL INFORMATION:
          4365
4365
4365
4500
602
580073
                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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408 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 467
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                          RESULT 3
US-08-342-268-69
Squence 69, Application US/08342268
Squence 69, Application US/08342268
Steam No. 5844072
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 69, Application US/09015968

Patent No. 6057425

GENERAL INFORMATION:
APPLICANT: Solsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,268

FILING DATE: 18-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/930,649

FILING APPLICATION DATA:

APPLICATION NUMBER: US 07/989,020

FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 102; DB 2; Best Local Similarity 100.0%; Pred. No. 4.1e-20; Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-UC 1206
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                      California
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122
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US-09-015-968-69
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                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                               1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
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                               Gaps
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                               0;
                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/08482279
Patent No. 5840498
GENBRAL INFORMATION:
APPLICANT: Selsted, Michael B.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 102; DB 2; Length 2408; 100.0%; Pred. No. 4.1e-20; Live 0; Mismatches 0; Indels 0
                               Indels
                                                                                                                                                                                 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                 468 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PILLIATION NUMBER: US/08/482,279
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                  ;
0
     Pred. No. 4.1e-20;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA.
PRIOR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
APTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REJERENGE/DOCKET NUMBER: 31,815
REFERENGE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
100.0%;
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Matches 102; Conservative
                               Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-482-279-69
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IBM PC compatible
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                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 102; DB 3; Length 2408; 100.0%; Pred. No. 4.1e-20; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTG 102
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07--UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 102; Conservative
                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                               CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-09-015-968-69
                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468
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408 CIGCITITITATACTAAGITIGGCATTATAAAAAAGCATTGCITATCAATTTGTTGCAACG 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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US-09-308-090-1

Sequence 1, Application US/09308090

Sequence 1, Application US/09308090

Sequence 1, Application US/09308090

SEMEMBAL INFORMATION:

APPLICANT: Ohl, Steephan

APPLICANT: Van Der Lee, Frederique

APPLICANT: Sijmons, Peter

APPLICANT: Sijmons, Peter

APPLICANT: Sijmons, Peter

APPLICANT: Sijmons, Peter

APPLICANT: Sijmons, Peter

FILE REFERENCE: MOS 57680

CURRENT APPLICATION NUMBER: US/09/308,090

CURRENT FILING DATE: 1999-05-14

EARLIER PILING DATE: 1996-11-18

EARLIER FILING DATE: 1996-11-18

MUMBER OF SEQ ID NOS: 10

SOFFWARDE OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 102; DB 4; Length 2408; 100.0%; Pred. No. 4.1e-20; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACAGGICACTAICAGICAAAAIAAAAICAITAITIGAIIIC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AACAGGICACIAICAGICAAAIAAAAICAITAITIGAITIC 509
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-NAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRAILON NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-849
INFORMATION FOR SEO ID NO: 69
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2408 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
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374 CIGCITITITATACTAAGITGGCATTATAAAAAGCATIGCTTATCAATTIGITGCAACG 433
                                                                                                                                                                                                                                             420 CIGCITITITIATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CIGCITITITATACTAAGTIGGCATTATAAAAAAGCATTGCTTATCAATTIGTIGCAACG
                                                                                                                                                                                                     1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                             Gaps
                                                                                                                                                           0
                                                                                                            Length 3484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3757;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                               61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                              480 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIIII 521
                                                                                                            100.0%; Score 102; DB 4;
100.0%; Pred. No. 4.3e-20;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-016-366A-13
Sequence 13, Application US/09016366A
Sequence 13, Application US/09016366A
Sequence 13, Application US/09016366A
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: LIMIBITORS
LOCATION: 3481..3484
OTHER INFORMATION: /codon_start= 3482
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBRS: US/09/016,366A
FILLING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 65
CORRESSONDEMESS:
ADDRESSEBE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFRAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3757 base pairs
                                                                                                                 Query Match
Best Local Similarity 100.
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 102; Conserv
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STREET: 600
TTW: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-016-366A-13
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US-09-380-090A-1
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                                                                                                                                                                                                                                  420 CHGCTTTTTTATACTAAGTTGGCATTATAAAAAAAGCATTGCTTATCAATTTGTTGCAACG 479
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                                                                                                                                                                                       1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                          Gaps
                                                                                                                                          0;
                                                                                                Length 3484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,090A
FILING DATE: 17-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: AURKNOWN>
                                                                                                                                                                                                                                                                            61 AACAGGTCACTATCAGTCAAAAAAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                         480 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC 521
                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/EP97/06472
FILING DATE: 18-NOV-1997
APPLICATION NUMBER: EP 96203213.2
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OHL, Stephan Andreas
SIJMONS, Peter Christiaan
KLEIN-VAN DER LEE, Frederique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SYN-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hale and Dorr LLP STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09380090A
Patent No. 655529
GENERAL INFORMATION:
APPLICANT: OHL, Stephan Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3484 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GODDIJN, Oscar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marianne
    ) NAME/KEY: CDS
; LOCATION: (3482)..(3484)
US-09-308-090-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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EARLIER FILING DATE: 1996-09-03
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                                                                                    5349
                                                                SEQ ID NO 7
                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 102; DB 2; Length 3757; Pred. No. 4.3e-20; 0; Mismatches 0; Indels 0
                                    434 AACAGGICACTAICAGICAAAATAAAATCAITAITIGAITIC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACAGGICACTATCAGICAAAIAAAAICAITAITIGAITIC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AACAGGICACTATCAGTCAAAATAAATCATTATTTGATTTC 475
                                                                                                                                           Sequence 19, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens,
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGGEN
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 74
CORRESSONDERGE ADDRESS:
ADDRESSEE Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILLE REFERENCE: 2121-1399
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,637
REFERNCE/DOCKET NUMBER: B0801/7090
TELECOMMINICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/09068101; Patent No. 6372960; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 102; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                  Arent: 600
                                                                                                       RESULT 9
US-08-978-404B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
TOPOLOGY:
US-08-978-404B-19
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                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
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4885 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 4826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (4246)..(4577)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "T-DNA of PTTS243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement((884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OCHER INFORMATION: Virus"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
MAMB/KRY: misc_feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin
OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: label = PB1, "promoter of El gene of rice (WO
OTHER INFORMATION: 92/13956)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATTON: Complement((98)..(331))
OTHER INFORMATION: label = 3'97, "region containing 3'
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (397\overline{0})..(4245)
OTHER INFORMATION: label = symb*; "improved barstar
                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: label = RB, "T-DNA right border"
FEATURE:
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; LOCATION: Complement((5325)..(5349))
; CTHER INFORMATION: label = LB, "T-DNA left border"
US-09-068-101-7
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100.0%; Score 102; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-20;
Matches 102; Conservative 0; Mismatches 0;
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Patent No. 6372960
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILE REPRENCE: 2121-139P
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (3970)..(4249
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520.31930X00
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFRENCE/DOCKET NUMBER: 520.:
TELECHMUNICATION INFORMATION:
TELECHMONE: 202-828-0300
TELEFAX: 202-828-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%;
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.0°
Matches 101; Conservative
                                                                                                                                                  19930224
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                    FILING DATE:
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US-08-021-667A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene of Nicotiana
                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement (139)..(317))
OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
OTHER INFORMATION: T-DNA"
                                                                                                                                                                    Description of Artificial Sequence: other nucleic acid, "plasmid pLH48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: Complement ((870) ..(1702))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: Complement((318)..(869))
OTHER INFORMATION: label = bar, "region coding for phosphinothricin
OTHER INFORMATION: acetyl transferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KRY: misc_feature
LOCATION: (2285)..(2560)
OTHER INFORMATION: label = synb*, "improved barstar DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: misc feature
LOCATION: (2561)..(2892)
OTHER INFORMATION: label = 3'chs, "region containing
OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1740)..(2284)
OTHER INFORMATION: label = FTA29, "promoter of TA29
OTHER INFORMATION: tabacum"
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100.0%; Pred. No. 4.6e-20;
iive 0; Mismatches 0;
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; Sequence 18, Application US/08021667A
; Patent No. 5434049
EARLIER FILING DATE: 1996-09-03
                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                  NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 102; Conservative
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NAME/KEY: misc_feature
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STATE: DC
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Best Local Similarity
                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                      FEATURE:
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                                                                                   LENGTH:
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43 CAGCTITITIATACTAAGTIGGCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 102
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; Sequence 18, Application US/08410544

; Patent No. 5607646

; GENERAL INFORMATION:

APPLICANT: Ckano, Kazunori

APPLICANT: Rambara, Hideki

; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

; TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 8.1e-20;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFFMALING SIGLEM: 1-2-505/m3-505
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 600, 1919 Pensylvania Ave., NW
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL RECOMBINANTLY SPIDER SILK ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR-9389-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: UTNE 15,1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-556-978B-78/c; Sequence 78, Application US/08556978B; Patent No. 6268169; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FAHRESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBIN
TITLE OF INVENTION: SPIDER SILK AN
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
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                                                                                                                                                                                                     101; Conservative
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Best Local Similarity 99.0
Matches 101; Conservative
          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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EDNESS: single
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                                                                                                                                                                 Query Match
Best Local Similarity
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CITY: WILMINTON
STATE: DELAWARE
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CLASSIFICATION:
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                                                                                                       ; ANTI-SENSE:
US-08-728-785A-18
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TELEFAX: 3
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Patent No. 587506
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGT
                                                                                                                                                                                                                                                                                                                                          Length 201;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Antonelli, Terry, Stout & Kraus
T: Suite 1800, 1300 No. 5817506th Seventeenth St.
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACAGGTCACTATCAGTCAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
FILING DATE: 10-OCT-1996
CLASSIPICATION: 437
PRIOR APPITCATION: 437
                                                                                                                                                                                                                                                                                                                                    Score 100.4; DB 1;
Pred. No. 8.1e-20;
0; Mismatches 1;
                      520.31930X00
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APPLICATION NUMBER: 08/410,544
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                REFERENCE/DOCKET NUMBER: 52
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
TELEPAX: 202-828-0380
  20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                    98.4%;
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                                                                                                                                                  LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                           TELEX: 248545
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.0°
Matches 101; Conservative
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REGISTRATION NUMBER:
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43 CAGCTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTGTTGCAACG 102
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                                                                                    1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
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    Length 201;
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                                                                                                                                                                                                                           103 AACAGGICACIAICAGICAAAIAAAAICAITAITIGAIIIC 144
98.4%; Score 100.4; DB 1;
99.0%; Pred. No. 8.1e-20;
ive 0; Mismatches 1;
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1007 MARKET STREET
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Pred. No. 1.3e-19;
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QV Ob

Search completed: September 9, 2004, 21:21:19 Job time: 23.4903 secs

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5; Search time 184.482 Seconds (without alignments) 3730.479 Million cell updates/sec
                                                                                                                                                                                                                                              1 totgttacaggtcactaata.....agcttttttatactaacttg 162
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                        9, 2004, 13:30:05
                                                                                   - nucleic search, using sw model
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                                                                                                                            September
                                                                                                                                                                                                                                 Perfect score:
                                                                                     OM nucleic
                                                                                                                                                                                                                                                         Sequence:
                                                                                                                              Run on:
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seq length: 0 seq length: 200000000 DB Minimum

Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

Searched:

6747726

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:* geneseqn2004s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003bs:* N_Geneseq_29Jan04:* geneseqn2003as:* geneseqn2002s:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adf61418 Bacteriop Acc85316 Recombina Acc44676 Artificia Abt16636 Artificia AAC9770 Bacteriop Acc83020 Bacteriop Acc83020 Bacteriop Acc431079 Rat neuro Acc4716 Plasmid p Abt16615 Artificia Aat18924 Plasmid p Aat30800 Vector pl Aaf30899 Vector pl Aaf30799 Vector pl Aaf30799 Vector pl Plasmid p Artificia Plasmid p Vector pl Vector pl Vector pl Vector pl E. coli a Acceptor E. coli a Bacteriop Recombina Acceptor Description Aaq45682 Aaf61421 Abq82141 Abq82141 Aaf61420 Abq82142 Abq82142 SUMMARIES AAF30800 AAF30801 AAF30798 AAF30799 AAQ45682 AAF61421 ABQ82142 ABQ82142 ABQ82141 ABQ82141 ABQ82141 AAF61418 ACC85316 ACC44676 ABT16636 AAF79770 ABQ80306 AAZ30709 ACC44716 **ABT16615** AAF61420 ACC83020 AAT18924 ΩĪ Query Match Length DB 17458 17476 17476 17681 4346 5670 5826 7652 17458 1469 1763 4909 5641 0.666 98.0 0.666 0.666 0.666 0.666 0.666 99 160.4 152.4 152.4 152.4 152.4 152.4 152.4 152.4 160.4 160.4 160.4 160.4 160.4 160.4 160.4 160.4 160.4 Score 160.4 160.4 160.4 No. 5 7 7 10 11 11 13 Result บ O υ

This invention describes a novel sequence-specific recombination (SSR) of DNA in a enkaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences

Abg82143 Acceptor

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Claim 3; Page 14; 24pp; German.

C 24 152.4 94.1 17681 6 ABQ82143 C 25 150.8 93.1 4204 3 AAC55522 C 26 150.8 93.1 4204 3 AAC55523 C 28 150.8 93.1 4470 3 AAC55521 C 28 150.8 93.1 4470 7 ABZ58767 C 29 150.8 93.1 4870 7 ABZ58767 C 29 150.8 93.1 4893 3 AAC55632 31 150.8 93.1 5584 7 ABZ58766 32 150.8 93.1 18691 6 ABQ82130 C 34 150.8 93.1 18691 6 ABQ82130 35 150.6 93.0 233 7 ACC5524 C 38 149.2 92.1 4165 3 AAC55522 40 149.2 92.1 4428 7 ABZ58768 41 149.2 92.1 4428 7 ABZ58768 44 149.2 92.1 4428 7 ABZ58768 44 149.2 92.1 4428 7 ABZ58769 44 149.2 92.1 4627 7 ABZ58770 45 149.2 92.1 4627 7 ABZ58770		Donor		Donor		Ada50329 Plasmid v		Aac55632 Donor pla			0			_		_		_	Abz58767 Destinati	Abz58769 Destinati	U2	Ada50329 Plasmid v
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226	94.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.0	93.0	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1
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ALIGNMENTS

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites. Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attR; ds. BP. 99DE-01041186. 99DE-01041186. AAF61420 standard; DNA; 162 (first entry) E. coli attR DNA fragment. WPI; 2001-246016/26. D, Escherichia coli. (DROE/) DROEGE DE19941186-A1. 30-AUG-1999; 30-AUG-1999; 01-MAR-2001. 05-JUN-2001 Droege P; AAF61420; RESULT 1 AAF61420 a

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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-541820/51.
                                                                                                                                                         ACC85316 standard;
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Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                                                                                                                                                            Unidentified.
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                                                                                                                                    TITIACAGIATIATGIAGICIGITITITATGCAAAATCIAAITTAATATATATTAATTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I. II) into a cell, using an integrase (int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) ector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sommatic gene therapy its derivatives. The method is applied more generally for gene theraps transfer to animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                                                                                                                                                                                                                                                                                Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                  TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                   Gaps
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                          Length 162;
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                                                 Indels
                                                                                                                                                           TAICATTTTACGTTCTCGTTCAGCTTTTTTATACTAGCTTG 162
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   75 T; 0 U; 0 Other;
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99.4%; Pred. No. 9.3e-25;
live 0; Mismatches 1;
                          DB 4;
                                      4.3e-25
                                               Mismatches
                         100.0%; Score 162; 100.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                          Bacteriophage lambda attP DNA fragment.
 A; 22 C; 22 G;
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Best Local Similarity 99.4%;
Matches 161; Conservative
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                                              Conservative
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                                 Local Similarity
Les 162; Conserv
 BP;
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 Sequence 162
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TITIACAGTATTATGTAGTAGTTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITITAAIATATIGAIATITA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
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plant; site-specific integration; nutrition; seed production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinase lambda integrase attP DNA recognition sequence
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                                                                                                                TAICALTITACGITTCTCGTTCAGCTTTTTTATACTAG 162
                                                                                                                                                            TALCATITIACGITICICGITCAGCITITITIAIACAGTIG 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160.4; DB 8;
Pred. No. 9.3e-25;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 35; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vegetable plastid transformation;
                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-2001; 2001DE-01063159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2002; 2002WO-EP014303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.08;
                                                                                                                                                                                                                                                                                                                              DNA; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemical production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŻ
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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 167

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Indels

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cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                     Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site, integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing artificial cannow preferably an ACes. (II) is useful for producing transgenic animal (e.g. a fish, insect, reptile, amphibian, arachind, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, and professibly a stem cell or an ambryonic coll continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a eukaryotic chromosome (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lindenbaum M, Greene A, Leung J, Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%; Score 160.4; DB 7; Length 282; 99.4%; Pred. No. 9.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 207; 272pp; English.
                                                                                                                                                                                                                                                  Murine rDNA PCR primer SEQ ID NO:72.
                                                               ACC44676 standard; DNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2001; 2001US-0294758P.
21-MAR-2002; 2002US-0366891P.
                                                                                                                                                                                     (first entry)
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Best Local Similarity 99.49
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perez C, Li
Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-140461/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200297059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus.
                                                                                                                                                                                     29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                         ACC44676;
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RESULT 4
                            ACC44676
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC comprises a heterologous nucleic acid encoding a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ERNA, EDNA, structural proteins, marker proteins, lagands, receptors, ribozymes, therapeutic proteins, and biopharmaccutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistence to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This polyanic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAAATATATGATATTTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                   blood factor, herbicide, stress, agronomical, nutrient quality;
bacterial artificial chromosome; BAC, yeast artificial chromosome; YAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Plant artificial chromosome; PAC; transgenic plant; vaccine;
                                                                      TATCATTITACGITICICGTICAGCITITITITATACTIG 162
                                                                                                                 135 TATCATTTTACGTTTCTCGTTTCACCTTTTTTTATACTAGTTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producing plant artificial chromosomes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 263-264; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perkins
                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2001; 2001US-0294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002WO-US017451
                                                                                                                                                                                                                                ABT16636 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-140436/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200296923-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                     03-APR-2003
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                                                                                                                                                                                                          ABT16636
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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

Pred. No. 9.3e-25; 0; Mismatches 1; Indels

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Primer, PCR; amplify; lambda phage; printer material; insertion;
deletion; single nucleotide polymorphism; sequencing; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 31-32; 91pp; English.
                                    ABQ80306 standard; DNA; 1469 BP.
                                                                                                              Lambda fragment in plasmid DNA.
                                                                                                                                                                                                                                                   24-SEP-2002; 2002WO-JP009766.
                                                                                                                                                                                                                                                                          25-SEP-2001; 2001JP-00291249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
                                                                                      (first entry)
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Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-354676/33.
                                                                                                                                                                                                                                                                                                    (DNAF-) DNAFORM KK.
                                                                                                                                                                                                                                                                                                                 RIKEN KK.
                                                                                                                                                                                                   WO2003027991-A1
                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                  applied on it.
                                                                                     27-JUN-2003
                                                                                                                                                                                                                          03-APR-2003
                                                                                                                                                                           Synthetic.
                                                              ABQ80306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                 (RIKE )
                          ABQ80306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibiotic resistance. The present sequence is the attP coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTA 120
                                                 Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                       74
               TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                       Attachment P region; attP; recombination; marker gene removal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 300
                                                                                                                        rarcaririracerirerestresecriririraraciaserie 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCATTTTACGTTTCTCGGTTCAGCTTTTTTTATACTAACTTG 162
                                                                                                  TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%; Score 160.4; DB 5 99.4%; Pred. No. 9.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                              Bacteriophage lambda attachment P region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig 3D; 25pp; English.
                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-2000; 2000WO-GB003543.
                                                                                                                                                                                                                                                                                                                                                                                                                  99GB-00021937
                                                                                                                                                                                    AAF79770 standard; DNA; 610
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                 Bacteriophage lambda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-266072/27
                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYLE-) UNIV LEEDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zubko E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                         WO200121780-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1999;
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Matches 161;
                                                                                                                                                                                                                                     29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001
                                                                                                                                                                                                               AAF79770;
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                       15
                                                61
                                                                         75
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                                                                                                                                                              RESULT 6
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The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 bp portion of lambda phage DNA contained in a plasmid. The amplified sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or colline applied on it. The printed material is useful in a method for synthesising DNA where the product of amplification and/or ligation is conversed and used for synthesising DNA where the product of amplification and/or ligation is collymorphism (SNP) and sequencing analysis, in a diagnostic method for determination of nucleotide insertion/deletion, or SNP analysis.

CC optionally, the cDNA and/or full-length cDNA is useful for the peptide, polymetrial expression. The printed material is useful in research applications, or for providing scientists with oligomer and/or polymetrs can an oligomer and/or polymetr can be obtained immediately and directly, without meed to make a request for it. The cligomers and/or polymers can be delivered and stored easily with reduced labour and time while eliminating the need to use special equipment or facilities. Thus, the printed material is a quick, efficient and inexpensive sample delivery system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       868 TITITACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITITAAIATITGAIAITIA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITIACAGIATIATGIAGICTGITITITATGCAAAATCIAATTTAATATATTTA
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Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 1469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 160.4; DB 7;
Pred. No. 9.2e-25;
0; Mismatches 1;
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ACC83020

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This sequence represents rat neuronal immediate early gene (IEG) cDNA clone R280. An IEG is a gene whose expression is rapidly increased immediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode as variety of proteins, including transcription factors, cytoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in, for example, learning memory, synaptic transmission, tolerance and neuronal pasticity. Neuronal IEGs, neuronal IEG protein products, cells cxpressing neuronal IEGs and antibodies against neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG responsivity to stimuli, such that the effect of the deficiency is minimised. The channel are an animal with a movement of expression of an IEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel genes and polypeptides, useful for treating conditions related to a deficiency in nIEG responsiveness to a stimulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 renginacaggicaeraanacearciaagiagingaricaragigacigearargrierg 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITIACAGIAITAIGIAGICIGITITITAIGCAAAAICTAAITITAAIAITGAIATITA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IEGs and protein products are useful in identifying compounds that modulate the expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIAIAITGAIAITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                 Immediate early gene; IEG; neuron; brain; function; growth factor; transcription factor; signal transduction; cytoskeletal protein; metabolic enzyme; learning; memory; synaptic transmission; tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160.4; DB 2; Denser-
Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity of IEG nucleic acids or proteins, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TATCATTTTACGTTCTCGTTCAGCTTTTTATACTAGCTTG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuner R,
                                       Rat neuronal immediate early gene cDNA clone R280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hiemisch H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE (BADI ) BASF-LYNX BIOSCIENCE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 114-115; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goetz B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
99.4%;
                                                                                                                                                                                                                                                                                                                                       99WO-US002462
                                                                                                                                                                                                                                                                                                                                                                                 98US-0074135P
                                                                                                                                                                                                                                                                                                                                                                                                         98US-0074518P
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                     neuronal plasticity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lanahan A,
Zhukovski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-590697/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 161; Conserv
05-JAN-2000
                                                                                                                                                                                                                                                                                                                                       05-FEB-1999;
                                                                                                                                                                                                                                                WO9940225-A1
                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         L2-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley PF,
Nikolich K,
                                                                                                                                                                                                                                                                                           12-AUG-1999.
                                                                                                                                                                                                      sb.
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                                                                                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for storing and/or delivering an oligomer and/or polymer applied on support. The support has oligomer and/or polymer applied on it, and is in the form of loose-leaf sheet or a card. The support is useful for storing and/or delivering an oligomer and/or polymer applied on it. The present sequence is Bacteriophage lambda DNA used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITIACAGIATIATGIAGICIGITITITIATGCAAAAICIAAITITAATATATTGATATITA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New support useful for storing and/or delivering an oligomer and/or polymer applied on support, has oligomer and/or polymer applied on it,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reretracadereacraniaceareratadracaricariacracacacararere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 160.4; DB 7; Length 1469; 99.4%; Pred. No. 9.2e-25; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                           Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAGGTTG 969
                         TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCATTITACGITICICGITCAGCITITITATACTAACTIG 162
  TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 162
                                                                                                                                                                                                                                                                                                                                       Oligomer storage; oligomer delivery; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 30-31; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and a loose-leaf sheet or a card.
                                                                                                                                                        ACC83020 standard; DNA; 1469 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ30709 standard; cDNA; 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2002; 2002WO-JP011492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35-NOV-2001; 2001JP-00339217
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.4
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-441569/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DNAF-) DNAFORM KK.
(HAYA/) HAYASHIZAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIKE ) RIKEN KK.
(DNAF-) DNAFORM K
                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003040360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y;
                                                                                                                                                                                                                                                   27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  928
    121
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ACC44716

AAZ30709/C ID AAZ3070 XX AC AAZ3070 XX

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4070 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTGTG 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and bipharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The proteins incomes in the protein and protein incomes the provides for resistance to diseases, insects, herbicides, or stress in a plant. The protein incomes and provides and protein and plant in the provides and protein and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the provides and plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant in the plant i
                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant artificial chromosome, PAC; transgenic plant; vaccine,
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents the DNA of a plasmid used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                 plasmid DNA SEQ ID No 26.
4190 TATCAITTTACGTTTCTCGTTCAGCTTTTTATACTAAGTTG 4231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 19; Page 255-256; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ε,
                                                                                                                                                                                                                                                                                                                                                                             Artificial plant chromosome related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perkins
                                                                                                                                                                                           BP.
                                                                                                                                                                                           ABT16615 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2002; 2002WO-US017451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2001; 2001US-0294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-140436/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200296923-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                   03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2002.
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nes 161;
                                                                                                                                                                                                                                                         ABT16615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perez C,
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                                                                                                                                 RESULT 11
                                                                                                                                                              ABT16615
                                   g
                                                                                                                                                                                                                                                      QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a ratificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection, crosprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 co ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4129
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                                                                                                                                                                                                                                         Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site, integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4070 rererracadereactaaraceareraacracarrearrearacacararrere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleming
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                                                                                                                                                                                     Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lindenbaum M, Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 244-245; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
ACC44716 standard; DNA; 4346 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2002; 2002WO-US017452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002US-0366891P
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                                                                                                                       (first entry)
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Shellard
                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda
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Best Local Simil
Matches 161;
                                                                                                                       29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002
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Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                             ACC44716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
Vibrio harveyi.
Bacteriophage lambda.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-290731/30.
                                                                            Local Similarity
Les 161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB20484
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coatings, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -35_signal
                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                     AAF30800;
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 palsei. This plasmid was used in the construction of the vector pFP510 which was used to express synthetic spider dragline variants, DP-1A.9 and DP-1B.9. palsei comprises a replication origin active in E. Coli, a selectable genetic marker which is a gene conferring resistance to mapicillin, sites for the restriction endonucleases BamHI and BglII with no essential sequences between them, and a third restriction site for perior pit, located within the selectable marker which produces cohesive ends incompatible with those produced by BamHI and BglII. The polypeptide monomers are variants based on a consensus sequence derived from the fibre forming regions of spider dragdline protein, esp. the natural protein 1 (Spidroin I) from Nephila clavipes. Synthetic analogues of DPI were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. DP-1A analogues are composed of a tandemly repeated 101 amino acid monomer which comparises four repeats which differ from the consensus sequence given in AAW06201, according to the pattern (1) (5): (1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-
              1130 TITTACAGIAITARGIAGICIGITITITARGCAAAATCIAATITAATAITGATATTTA 4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alanine sequence is deleted, so also is the surrounding sequence encompassing ASRGGLGGQGAGAGG; (3) aside from the poly-alanine sequence, deletions usually encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and (5) a repeat in which the entire poly-alanine in the same sequence; and (5) a repeat in which the entire poly-alanine is deleted is generally preceded by a repeat containing six alanine residues. The proteins way be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films,
                                                                                                                                                                                                                                                                                                   Spider; dragline protein; variant; monomer; polymer; circular; fibre forming reglon; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating; ss.
TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents the complete nucleotide sequence of the plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells.
                                                                                   4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAAGTTG 4231
                                                           TAICATTITIACGITICICGITICAGCITITITIATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                        AAT18924 standard; DNA; 4909 BP
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                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                       Plasmid pA126i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9429450-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1994;
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                                                                                                                                                                                                                                       17-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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ID AAT18
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2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                                                                                                                                                                                TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTTA 120
                                                                                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a regulatory element capable of directing or regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
                                                                                                                  0;
                                           99.0%; Score 160.4; DB 2; Length 4909; llarity 99.4%; Pred. No. 9.2e-25; Conservative 0; Mismatches 1: Indels n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2396 TATCATTTTACGTTTCTCGTTTCAGCTTTTTATACTAAGTTG 2355
                                                                                                                                                                                                                                                                                                                                                                                                                     TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAGCTTG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector plasmid pJMF3 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Lac repressor binding site"
1895. .2014
/*tag= e
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note= "CAP-cAMP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Lac promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF30800 standard; DNA; 5641 BP
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1857. .1883
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/product= "lacZ-chitobiase fusion"

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                                                                                          The present sequence is that of vector plasmid pJMF3, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lac2—alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chitcbiase gene plasmid pUC19) fused in-frame to the Vibrio harveyi chitcbiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitcbiase enzyme as a reporter. A claimed reporter gene construct comprises pJMF3. The invention also comprises expression vectors which express the cytoplasmic form of chitcbiase. Methods are provided for: characterizing a promoter; identifying a regulatory atement capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosiales as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGATATTTA 120
transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4703 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAICALTITIACGITICICGITICAGCITITITIATACTAAGIIG 4864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCATITIACGITICICGTICAGCITITITIATACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Lac repressor binding site"
895. .2014
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160.4; DB 4
Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note = "CAP-cAMP binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function= "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function= "Lac promoter"
                                                           Example 1; Page 32-34; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
AAF30801 standard; DNA; 5670 BP.
XX
AC AAF30801;
XX
DT 11-SEP-2003 (revised)
DT 21-JUN-2001 (first entry)
XX
XX
XX
Chitobiase; reporter gene; LacZ genes, Vibrio harveyi.
S Bacteriophage lambda.
S Chimeric.
XX
XX
CH Chitobiase; reporter gene; LacZ genes, Vibrio harveyi.
S Bacteriophage lambda.
S Chimeric.
S Chimeric.
S Chimeric.
S FT Protein_bind 1783. .1810
FT Protein_bind 1783. .1810
FT Protein_bind 1783. .1810
FT -35_signal 1820. .1826
FT -10_signal 1845. .1850
FT FT Chitophage lambda.
FT T Theorem 1845. .1850
FT T Theorem 1845. .1833
FT T Theorem 1857. .1883
FT FT Protein_bind 1857. .1883
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Best Local Similarity 99.49
Watches 161; Conservative
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phage lambda attP and the lac promoter with the first 21 amino acids of lac2-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chitobiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pUMF4. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transformation, and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIACAGIAITAIGIAGICIGIIITITIAIGCAAAICIAAITIAAIAIAITIGAIAITIA 4922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIACAGIAITAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIAITAITGAJAITITA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is that of vector plasmid pJMF4, which includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitobiase; reporter gene; dnaA gene; promoter; vector; pDYK9; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160.4; DB 4; Length 5670; Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCATTTTACGTTTCTCGTTCAGCTTTTTTTTACTAAGTTG 4880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 34-36; 44pp; English.
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                                                                                                                                                02-AUG-2000; 2000WO-US021048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 161; Conservative
                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-290731/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB20484.
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Chimeric.
WO200127322-A2
                                                                                                                                                                                                                        13-OCT-1999;
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21-JUN-2001
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                                                                        19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                Zyskind J;
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The present sequence is that of vector plasmid pDYK9, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia coli dnaA promoter in plasmid pACYC184. pDXK9 was used to assess the regulation of the dnaA gene using chitobiase as a reporter enzyme. A claimed reporter gene construct comprises pDYK9. The invention relates to enzyme as a reporter. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene system in that it is not necessary to engineer many host cells.
                                                                                                                                                                                                                                                                                              Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 29-30; 44pp; English.
                                                                                                02-AUG-2000; 2000WO-US021048.
                                                                                                                                      99US-0159221P
                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                           WPI; 2001-290731/30
                      WO200127322-A2.
                                                                                                                                      13-OCT-1999;
                                                           19-APR-2001
                                                                                                                                                                                                                    Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            field)
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Sequence 5826 BP; 1574 A; 1346 C; 1389 G; 1517 T; 0 U; 0 Other; 0; tch 39.0%; Score 160.4; DB 4; Length 5826; al Similarity 99.4%; Pred. No. 9.2e-25; 161; Conservative 0; Mismatches 1; Indels 0; Query Match Best Local Similarity Matches 161; Conserv

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Search completed: September 9, 2004, 18:05:41 Job time: 185.482 secs

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Sequence 9, Appli
                                                                                                                                                                                                                                                    9, 2004, 19:34:38; Search time 128.856 Seconds (without alignments) 3982.858 Million cell updates/sec
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Sequence 57,
Sequence 57,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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7 US-10-627-711-9

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US-09-970-921-10

US-10-403-221-17

US-10-310-695-14

US-10-310-695-14

US-10-161-403-72

US-10-245-771-8

US-10-245-277-57

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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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102
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                                                                                                                                                                                                                                                             Run on:
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13	13	T -	0 6	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	10	13	16	72	13	15	15	15	15	12	
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100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100	93.8	93.8	93.8	92.2	92.2	92.2	92.2	92.2	92.2	
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APPLICANT: DROGE, PETER
APPLICANT: ENENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REFERENCE: DEBE: 0.19  
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
                               ; Sequence 15, Application US/10310695; Publication No. US20040110293A1; GENERAL INFORMATION:
US-10-310-695-15
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ALIGNMENTS

SOFTWARE: Patentin Ver. 2.1 ORGANISM: Escherichia coli SEQ ID NO 15 US-10-310-695-15 TYPE: DNA

1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60 Gaps 0 Length 102; Indels 100.0%; Score 102; DB 17; 100.0%; Pred. No. 1.6e-18; Live 0; Mismatches 0; 102; Conservative Best Local Similarity Query Match Matches

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1 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102 RESULT 2 US-10-627-711-9 g ð

; Sequence 9, Application US/10627711; Publication No. US20040115812A1; GENERAL INFORMATION:

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Gaps

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Length 3049; Indels

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2398 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 2457
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NAME/KEY: misc_feature

LOCATION: Complement(1)..(25))

OTHER INFORMATION: label = RB, "T-DNA right border"

NAME/KEY: misc feature

LOCATION: Complement(199)..(331))

OTHER INFORMATION: label = 3'97, "region containing 3' untranslated OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
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LOCATION: Complement (1312)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin
OTHER INFORMATION: acetyl transferase"
NAME/KEY: misc feature
LOCATION: complement (1844)..(2258)
OTHER INFORMATION: label = P355, "355 promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
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OTHER INFORMATION: label = PE1, "promoter of E1 gene of 1
OTHER INFORMATION: 92/13956)"
NAME/KEY: misc. feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*; "improved barstar DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 102; DB 13; Best Local Similarity 100.0%; Pred. No. 5.1e-18; Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09970921
Patent No. US20020133845A1
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Barstar Gene
FILE REPRENENT 12012 1200109/970,921
CURRENT APPLICATION NUMBER: US/09/970,921
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
CURRENT APPLICATION NUMBER: US/10/432,148
CURRENT FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 3049
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                                                                                                                                                                                                                                                                                                                                NAME/KEY: mRNA
LOCATION: (2928)..(3049)
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: TATA signal LOCATION: (2877). (2883)
                                                                                                                                                                                            ORGANISM: Beta vulgaris
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LOCATION: (2281)..(3969
                                                                                                                                                                                                                                                 NAME/KEY: promoter
LOCATION: (1)..(2998)
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US-09-970-921-7/c
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                                                                                                                                                                        TYPE: DNA
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     APPLICANT: YANG, Shuwei
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
TITLE OF INVENTION: SCREENING OF CDNA CLONES
FILE REFERENCE: 51236US
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Publication No. US20030226164A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suttie, Janet Louise
APPLICANT: Suttie, Janet Louise
APPLICANT: Chilton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: de Framond, Anic
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 70005USPS
CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 102; DB 17;
100.0%; Pred. No. 1.6e-18;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e-18;
iive 0; Mismatches 0;
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TITLE OF INVENTION: tissue specific promoter
FILE REFERENCE: tissue specific promoter 1
                                                                                                        CURRENT APPLICATION NUMBER: US/10/627,711
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: 60/398,589
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bacteriophage lambda
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: primer US-10-627-711-9
                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 102; Conserv
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US-10-432-148-4
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US-10-403-232-173
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LENGTH: 243
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OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (256I)..(2892)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                                                                                                   0; Gaps
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NAME/KEY: misc feature
LOCATION: Complement((39)..(317))
OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium OTHER INFORMATION: T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement (318)..(869))
OTHER INFORMATION: label = bar, "region coding for phosphinothricin
OTHER INFORMATION: acetyl transferase"
NAME/KEY: misc feature
LOCATION: Complement (1870)..(1702))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
NAME/KEY: misc feature
LOCATION: (1740)..(2284)
                            COCATION: (4246)...(4577)
COTHER INFORMATION: label = 3'chs, "region containing 3' untranslated OTHER INFORMATION: end of chalcone synthase gene"
NAME/KEY: misc_feature
COMPLEMENTION: Complement((5325)..(5349))
COTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7
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                                                                                                                                                                                                                                                Length 5349;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: label = synb*, "improved barstar DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                           ; Score 102; DB 9;
; Pred. No. 6.2e-18;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09970921
; Patent No. US20020133845A1
; GENERAL INFORMATION:
   APPLICANT: Frank Michiels et al.; TILLE OF INVENTION: Improved Barstar Gene; FILE REFERENCE: 2428-0108P
   CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 102; Conservative 0
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LOCATION: (2285)..(2560)
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        NAME/KEY: misc_feature
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LENGTH: 5611
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3200 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 3141
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APPLICANT: ENENKEL, BARBARA
TITLE OF INVENTION: SQUENCE SPECIFIC DNA RECOMBINATION IN BUKARYOTIC CELLS
FILE REFERENCE: DEBE:019US
CURRENT APPLICATION NUMBER: US/10/310, 695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
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US-10-403-232-173
Sequence 173, Application US/10403232
PUBLICATION NO. US20030226164A1
GENERAL INFORMATION:
APPLICANT: Suttie, Janet Louise
APPLICANT: Cullton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
FILE REFRENCE: 70005USPS
CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PATENTIN version 3.2
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Pred. No. 5.9e-18;
0; Mismatches 1; Indels
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Pred. No. 5.9e-18;
0; Mismatches 1; Indels
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                                                          61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10310695 Publication No. US20040110293A1 GENERAL INFORMATION:
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Best Local Similarity 99.0%;
Matches 101; Conservative
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Best Local Similarity 99.0%;
Matches 101; Conservative
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ORGANISM: Artificial Sequence
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SEQ ID NO 2
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Sequence 72, Application US/10161403 Publication No. US20030119104A1 ABPRICAL INFORMATION: Behard APPLICANT: Perkins, Edward
                                                                                                                                                                                Lindenbaum, Michael
Greene, Amy
Leung, Josephine
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99.0%;
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Best Local Similarity 99.0%
Matches 101; Conservative
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US-10-161-403-72
                                                                                                                                                         Perez, Carl
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Publication No. US20040115812A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
TITLE OF INVENTION: SCREENING OF CDNA CLONES
                                                                                                                                                      Sequence 14, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FOR A PAPLICANT:
GENERAL SMEMKEL, BARBARA
TITLE OF INVENTION:
FILE REFERENCE:
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Pred. No. 6e-18;
0; Mismatches 1; Indels 0;
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202 AACAGGICACTATCAGICAAAATAAAATCATTATTIGATITC 243
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CURRENT APPLICATION NUMBER: US/10/627,711
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: 60/398,589
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Bacteriophage lambda
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Best Local Similarity 99.04
Matches 101, Conservative
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Best Local Similarity 99.0
Matches 101; Conservative
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                                                                                                         RESULT 9
US-10-310-695-14
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RESULT 11 US-10~161-403-72

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156 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 215
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APPLICANT: Worley, Paul F.
APPLICANT: Morley, Paul F.
APPLICANT: Landan, Anthony
APPLICANT: Landan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Goetz, Bernard
APPLICANT: Kuner, Rohini
APPLICANT: Kuner, Rohini
APPLICANT: Sidrid
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APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERRNCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR PLILING DATE: 2001-05-30
PRIOR PLILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTERO for Windows Version 4.0
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Publication No. US20030203840A1
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1763)
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LENGTH: 1763
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US-09-245-277-57/c
Sequence 57, Application US/09245277
Publication No. US20030211984A1
GENERAL INFORMATION:
APPLICANT: Worley, Paul F.
APPLICANT: Landan, Anthony
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: JHU1530-3
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APPLICANT: Worley, Paul F.
APPLICANT: Lanahan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Heimisch, Holger
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Zhukovski, Eugene
IITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
                                                                                                                                                                                                  1 CIGCITITITIATACTAAGTIGGCAFTATAAAAAAGCAFIGCITAFCAAT
                                                                                                                                                  1; Indels
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                                                                                                  Query Match 98.4%; Score 100.4; DB 1:
Best Local Similarity 99.0%; Pred. No. 1.2e-17;
Matches 101; Conservative 0; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/245,277

CURRENT FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: 60/074,518

PRIOR APPLICATION NUMBER: 60/074,135

PRIOR APPLICATION NUMBER: 60/074,135

PRIOR PILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/10792481 Publication No. US20040152658A1
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OTHER INFORMATION: y = C or T

OTHER INFORMATION: n = A,T,C or G
; OTHER INFORMATION: y = C or T; OTHER INFORMATION: n = A, T, C or G US-09-244-805-57
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ORGANISM: Eukaryote
FEATURE:
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US-10-792-481-57/c
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SEQ ID NO 57
LENGTH: 1763
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APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLESMIDS, STRAINS, AND METHODS OF USE
FILE REPERENCE: 250.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 10496/004001

CURRENT APPLICATION NUMBER: 02/10/792,481

CURRENT FILING DATE: 2004-03-02

PRIOR APPLICATION NUMBER: US/09/244,805

PRIOR FILING DATE: 1999-02-05

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1998-02-12

PRIOR PELING DATE: 1998-02-16

PRIOR PELING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FRACESQ for Windows Version 4.0

SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(1763)
OTHER INFORMATION: y = C or T
OTHER INFORMATION: n = A, T, C or G
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Best Local Similarity 99.0%;
Matches 101; Conservative
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ORGANISM: Eukaryote
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Search completed: September 10, 2004, 00:14:08 Job time: 129.856 secs

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12, Appl
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57, Appl
33, Appl
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88, Appl
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162
1 tctgttacaggtcactaata......agctttttatactaacttg 162
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.. /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
.. /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
.. /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
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.. /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*
.. /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-453-702B-50
US-08-021-667A-17
US-08-1410-544-17
US-08-453-702B-66
US-08-453-702B-66
US-08-410-544-18
US-08-72B-785A-18
US-08-790-988-1
US-09-790-988-1
US-09-790-988-1
US-09-790-988-1
US-09-790-988-1
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US-08-998-416-595
US-10-204-708-89
US-10-204-708-88
US-10-204-708-88
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US-10-204-708-57
US-10-204-708-27
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US-10-204-708-33
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Maximum Match 1008
Listing first 45 summaries
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                                                                                     - nucleic search, using
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Maximum DB seq length: 2000000000
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Match Length DB
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5455
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37.6
37.4
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36.4
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                                                                                     OM nucleic
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                                                                                                                                                                                                             Title:
Perfect
                                                                                                                              Run on:
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Sequence 24, Appl Sequence 24, Appl Sequence 22, Appl Sequence 12, Appl Sequence 11, Appl Sequence 134, Appl Sequence 14, Appl Sequence 17, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 39, Appl Sequence 39, Appl Sequence 2779, Appl Sequence 179, Appl Sequence 179, Appl Sequence 18, Appli Sequence 179, Appli Sequence 179, Appli		4909; 0; Gaps 0;
<u> </u>		Length Indels
C 28 35 21.6 1493 1 US-08-340-820-24 C 29 35 21.6 1493 1 US-08-593-535-24 C 30 35 21.6 1493 1 US-08-593-535-24 C 31 35 21.6 1493 1 US-08-593-535-24 32 35 21.6 13425 4 US-09-976-594-856 33 34.8 21.5 164976 4 US-08-916-421B-1 34 34.8 21.5 6243 2 US-09-916-421B-1 35 34.4 21.5 6243 2 US-09-056-075-1 37 34.4 21.2 1495 3 US-09-056-075-1 38 34.2 21.1 1452 4 US-09-227-357-119 40 34.2 21.1 1452 4 US-09-227-357-119 41 34.2 21.1 19513 4 US-10-204-708-8 C 43 34 2 21.1 19513 4 US-0-227-357-119 C 44 34 2 21.1 19513 4 US-0-227-357-119 C 45 33.8 20.9 998 3 US-09-134-000C-2779 C 45 33.8 20.9 998 3 US-09-122-400B-5	RESULT 1 US-08-556-978B-78/C US-08-556-978B-78/C Sequence 79, Application US/08556978B Patent No. 6268169 Fatent No. 6268169 Fatent No. 6268169 Fatent No. 6268169 Fatent No. 6268169 Fatent No. 6268169 FAPLICANT: FARNESTOCK, STEPHEN F. TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS NUMBER OF SEQUENCES: 107 STREET: 1007 WARKET STREET CITY: WILMINTON STREET: 1007 WARKET STREET CONDERSON: UNITED STATES OF AMERICA ZIP: 1999 COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: UNITED STATES OF WINDOWS 95 SOFTWART WEDEL OF WORD FOR WINDOWS 95 SOFTWART APPLICATION DATH: US/08/556,978B FILING DATE: UNIMER: 08/077,600 FILING DATE: UNIMER: 08/077,600 FILING DATE: UNIMER: 08/077,600 FILING DATE: UNIMER: 08/077,600 FILING DATE: UNIMER: 08/077,600 FILING DATE: UNIMER: 08/077,600 APPLICATION NUMBER: 08/077,600 FILING DATE: UNIMER: 08/077,600 FILING DATE	Query Match 99.0%; Score 160.4; DB 3; L Best Local Similarity 99.4%; Pred. No. 1.6e-28; Matches 161; Conservative 0; Mismatches 1; I

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APPLICATION NUMBER: US/07/590,988A
                                                                                                                                                                                                                                                                                               TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 base pairs
TYPE: NUCLBIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
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Welch, Rod
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Best Local Similarity 99.45
Matches 161; Conservative
                                                19901001
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COUNTRY: US
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US-07-590-988A-1
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US-09-453-702B-50
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2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
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                                                                 61 TITIACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
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Factor No. 6205085
Factor No. 6205085
GENERAL INFORMATION:
FILLS OF INVENTION:
FILLS PREFERENCE:
FILLS REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6043;
                                                                                                                                                                                                                                       2396 TATCATTTACGTTCTCGTTCAGCTTTTTTATACTAAGTTG 2355
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                                                                                                                                                                                                     121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAACTTG 162
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MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160.4; DB 4;
Pred. No. 1.6e-28;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blattner, Frederick R. TITLE OF INVENTION: DNA Sequencing Vector with TITLE OF INVENTION: Reversible Insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
COUNTE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53701
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GENERAL INFORMATION:
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99.4%;
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Matches 161; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles a:
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US-09-630-929-4/c
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US-07-590-988A-1
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5993 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 6052
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NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7652;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160.4; DB 1
Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Other nucleic acid, DESCRIPTION: synthetic recombinant plasmid HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: Chiknown>
PRIOR APPLICATION: Chiknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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STREET: 1 South Pinckney Street
CITY: Madison
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FILING DATE: 04-DEC-1998
                                                                                                                           9629691682
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
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Gaps

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102 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATCTGTTGTG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08410544
; Sequence 17, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
    APPLICANT: Okanbara, Hideki
    TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
    TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
    TITLE OF INVENTION: METHOD USING SAME
    NUMBER OF SEQUENCES: 18
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Antonelli, Terry, Stout & Kraus
    STREET: Suite 600, 1919 Pensylvania Ave., NW
    CORNER OF SEQUENCES: 19
    CORNER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                  162 rritacagrafiangragicigirrirrangcaaarcr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                                                                                                                                                                                                                         61 TITTACAGIATIATGIAGICIGITITITATGCAAATCI
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                                                                                                        Score 97.4; DB 1;
Pred. No. 3.1e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-828-0300
TELEFAX: 202-828-0380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                               60.1%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 200 bace
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 98; Conservative
                                                                                                                                                                              Conservative
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                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                         , ANTI-SENSE:
US-08-021-667A-17
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US-08-410-544-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 38584;
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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: TELY, DAVID T.
REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104.6; DB 4;
Pred. No. 9.9e-16;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE M
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: AHCONGIL, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520.31930X00
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
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APPLICANT: Okano, Kazunori APPLICANT: Kambara, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
CULE TYPE: DNA (genom
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Best Local Similarity 83.2%;
Matches 119; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEX: 440280/248545
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
                                                                                                                                                                                       LENGTH: 38584
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Best Local Similarity
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STRANDEDNESS:
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US-08-021-667A-17
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Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
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                                                                                                            Sequence 17, Application US/08728785A
Patent No. 5817506
GENERAL INFORMATION:
CARADIL REMARTION:
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSE: Antonelli, Terry, Stout & Kraus
STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                     162 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCT 200
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              61 TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCT 99
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TELECOMPUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6600
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                               ADDRESSEE: Antone STREET: Suite 180 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
Matches 98; Conserv
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US-08-728-785A-17
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                                                                                                 US-08-728-785A-17
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RESULT 8 US-09-453-702B-66/c ; Sequence 66, Application US/09453702B

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60 GITITACAGIATTATGIAGICIGITITITATGCAAAATCIAATTIAATATATATATATTT 119
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; Patent No. 5434049
; GENERAL INFORMATION:
APPLICANT: OKANO, Kazunori
APPLICANT: Kambar, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                         ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                             TITLE OF INVENTION: No. 6365723el Sequences of E. NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-453-702B-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                        Nicole T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                      Perna,
Plunkett, Guy
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SEQUENCE CHARACTERISTICS
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Matches 107; Conservative
Burland,
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Arlington
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ZIP: 22209
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STREET: Su
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STATE:
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US-08-410-544-18

Sequence 18, Application US/08410544

Patent No. 5607646

GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Ambara, Hideki
ITILE OF INVENTION: POLYNUCLECTIDE CAPTURING TIP AND
ITILE OF INVENTION: POLYNUCLECTIDE PREPARATIVE METHOD AND DETECTION
ITILE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pensylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AATITAATATATTATATTATATCATTITTACGTTTCTCGTTCAGCTTTTTTATACTAAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.9%; Score 61.4; DB 1; Length 201; 98.4%; Pred. No. 5.1e-06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                        COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAPLICATION NATA:
APPLICATION NUMBER: US/08/021,667A
FILLING DATE: 19930224
             ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                    520.31930X00
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 520.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20.2-828-0300
TELEFAX: 20.2-828-0380
TELEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          FILING DATE: 19930224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-021-667A-18
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                                                                               STATE: DO COUNTRY: ZIP: 2001
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100 AATTTAATATTTTATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAC 159
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APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 201;
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Suite 1800, 1300 No. 5817506th Seventeenth St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.4; DB 1;
Pred. No. 5.1e-06;
0; Mismatches 1;
CLASSIFCATION: 435
PRIOR APPLICATION BYA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: TEATY, DAVIG T.
RESISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-828-03300
TELEFAX: 202-828-03300
TELEFAX: 202-828-03300
TELEFAX: 202-828-0310
TELEFAX: 202-828-0310
TELEFAX: 202-828-0310
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,544
FILING DATE: 21-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION PUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTONEY/AGAIT INFORMATION:
NAME: Terry, DAVIG T:
REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08728785A Patent No. 5817506 GENERAL INFORMATION:
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MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
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Best Local Similarity 98.4%;
Matches 62; Conservative
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Query Match
Best Local Similarity 54.77
Matches 76; Conservative
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                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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US-08-487-826B-13
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US-09-790-988-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATAABAB, HIDEAT
APPLICANT: WATAABAB, HIDEAT
APPLICANT: HATTORI, WASAHHRA
APPLICANT: ARAZAHIRA
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0129
CURRENT PILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTH VET. 2.1
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                                                                                                                                                                                                                                                                            Length 201;
                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                         37.9%; Score 61.4; DB 1;
98.4%; Pred. No. 5.1e-06;
live 0; Mismatches 1;
   520.31930X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09790988
Patent No. 6632935
               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
REFERENCE/DOCKET NUMBER:
                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.49
Matches 62, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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US-08-487-826B-13/c
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US-08-728-785A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-790-988-1
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// Sequence 13, Application US/08487826B
// Patent No. 5993827
// GENERAL INFORMATION:

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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15819 Artraaaraaartririrrarigrarararararirrirrirraaacarrirriraaara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 ATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTGTTTTACAGTATTATGTAGTCTG
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Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
APPLICATION DAPA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435.
ATTORNEY/AGENT INFORMATION:
NAME: BEFRAFILON
NAME: 1 BFRAFILON
NAME: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                      16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.2; DE
Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH121.001CP1
                                                                                                                                                                                                                                                                                              STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                             Knobbe Martens Olson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15699 ATGATATATTTTTTTTT 15681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.6%;
54.7%;
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nucleic acid
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451315 richtaaaaactririgricaararaaararirrirtaagaaragariricrirriraccaa 451256
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                                                                                                                                                                                                                                                                                                               12 TCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTTTTTACAGTAT 71
                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATVORI, WASAHIRA
APPLICANT: HATVORI, VOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
TITLE REFREENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 7786
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                                                                                                                                                                                                                            Query Match 23.2%; Score 37.6; DB 4; Length 640681; Best Local Similarity 54.3%; Pred. No. 2.3; Matches 76; Conservative 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.1%; Score 37.4; DB 4; Length 7786; Best Local Similarity 57.1%; Pred. No. 1.9; Matches 68; Conservative 0; Mismatches 51; Indels 0
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; PRICR APPLICATION NUMBER: JP2000-107160
; PRICR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
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Patent No. 6632935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-2
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AQ991774 REC02039F
AQ991791 REC02368F
AQ990809 REC01638
AQ990869 REC01706
                                                                                                                                                                                   September 9, 2004, 17:30:16; Search time 1308.61 Seconds (without alignments) 3696.811 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
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	7		ς.	787	14	116	47604	AGENCOURT
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υ	σ	40	86.9	756	28	AQ991732	1732	Rfc00380F
	10	37.	ď.	777	14	4768	17686	AGENCOURT
υ	1.1	34.	е С	583	14	3388	33882	OSTR013H1
υ	12	33.	2	395	28	9130	91303	Rfc02205
υ	13	29.	0	393	14	98	33984	OSTR015E7
υ	14		6	769	28	47	170	Rfc01245
υ	15	26.	7.	764	28	187	378	Rfc01715
	16	23.	9	487	14	523	230	OSTR151B2
υ	17	121	4.	556	28	AQ991338	AQ991338	Rfc02255
υ	18		0	743	α	AQ990346	346	Rfc01106
O	19	114.4	0	472	m	739	398	NF104D07I
υ	20	14.	0	473	m	BQ156404	104	NF092E03I
υ	21		٥.	758	ω	AQ991690	969	Rfc01924F
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U	27	8		808	œ	AQ990388	38	Rfc01153
	28	œ.	4.	810	4	CF347481	181	AGENCOURT
υ	59	ġ.	ë.	719	æ	AQ991352	352	Rfc02270
υ	30	Η.	Ö	715	œ	AQ991358	358	R£c02278
υ	31	9	7.	695	8	AQ991039	339	Rfc01894
υ	32	ė,	7.	384	N	BI174407	101	OSTF043E1
υ	33	74.6	ė.	167	В	AQ990301	301	Rfc01055
υ	34	7.	ij.	597	N	B1422679	22679	EST533345
	35	7.	Ή.	800	4	CF347726	9	AGENCOURT
υ	36	ď		764	œ	AQ990110	0	Rfc00827
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RESULT 1 A0991774/C LOCUS DEFINITION	AQ991774 T70 bp DNA linear GSS 14-AUG-2000 Rfc02039F Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG02039F, genomic survey sequence.
ACCESSION VERSION KEYWORDS	AQS91774.1 GI:9650368 GSS.
SOURCE ORGANISM	Photorhabdus luminescens Photorhabdus luminescens Bacteria; Proteobacteria; Enterobacteriales; Barterhardariaceae, Dhotorhabdus
REFERENCE AUTHORS	1 (bases 1 to 770) ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. Agonomic sample sequence of the entomorathogenic harterium
TILLE JOURNAL MEDLINE PUBMED	A genomic sample sequence of the encomparize bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000) 20378633 10919786
COMMENT	Contact: ffrench-Constant RH Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621

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Query Match
Best Local Similarity
Matches 162; Conserv
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                                                                                                                                                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium bhotorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae; Photorhabdus.
              This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. Seg primer: M13 Reverse Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Desric@bath.cc.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASIX, BLASIX and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primar: M13 Reverse
class: Shotgun.
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Photorhabdus luminescens genomic clone PLG02368F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                   /db_xref="taxon:29488"
/clone="PLG02039F"
/dow_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                           organism="Photorhabdus luminescens"
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; Pred. No. 7.3e-22;
0; Mismatches 0;
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Department of Biology and Biochemistry
University of Bath
South Baliding, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="W14"
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Smail: bssrfc@bath.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 100.0%;

Matches 162; Conservative 0
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AQ991791/c
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                                                                                                                                                                                                     library" /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ITTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01638, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 ITTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                             /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:29488"
/clone="pEQ01638"
/dev_stage="primary_phase_variant"
/clone_lib="Photorhabdus_luminescens_strain_W14_M13_
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organism="Photorhabdus luminescens"
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 162; DB 28;
100.0%; Pred. No. 7.2e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Photorhabdus.
                  /mol_type="genomic DNA"
/strain="W14"
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/strain="W14"
                                                                                 /db_xref="taxon:29488"
/clone="PLG02368F"
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1, .712
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                                                                                                                                                                                                                                                                                                                                                                                                                    162; Conservative
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BST 08-DEC-2002

ORIGIN

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Nikaido,I., Cosato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Sichonach,C., Golobori,T., Baldarali,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothai,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Grimmond,S., Gustinoich,S., Hirokawa,N., Jackson,I.J., Javvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.W., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.W., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Lee,Y., Bertea,G., Percoscole,G., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Reed,D.J., Reid,J., Ramechandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelinh,A., Schoulder,C., Semple,C.A., Tasdale,R.D., Tomita,W., Verando,R., Wagner,L., Wanlestedt,C., Wang,Y., Watanabe,Y., Hayatsu,M., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Funda,A., Hashizume,W., Imotani,R., Indean,R., Indean,R., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,B., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
                                                                                                                                                                                        BY115594 EST 08-DEC-2003
BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus
musculus cDNA clone L430040C03 5', mRNA sequence.
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The Institute of Physical Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                            481 TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTTGTTTTA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 299)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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URL.http://genome.gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
                       6 TACAGGICACTAATACCATCTAAGTAGTIGATTCATAGTGACTGCATATGTTGTGTTTTTA
                                                                                                                                                                                                                                                   126 TITIACGITICICGITCAGCITITITATACTAACTIG 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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BY115594.1 GI:26226695
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Fax: 81-45-503-9216
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                  /note=""Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                        09
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01706, genomic survey
                                                                                                                                                                                                                                                                                                          591 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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library"
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                                                                                                                                   Score 160.4; DB 28; Length 712;
Pred. No. 1.5e-21;
0; Mismatches 1; Indels 0;
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Department of Biology and Biochemistry
University of Bath
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/strain="W14"
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/clone="PLG01706"
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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1. .708
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GSS.
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                                                                                                                                   ch 18 Similarity 99.4%; 161; Conservative (
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SOURCE

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Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2010)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Musus Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Further decalis.
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AGENCOURT_15225345 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001697
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(Dases 1 to 827)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone lib="RIKEN full-length enriched, 18 days embryo
whole body"
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Bldg. 31 RmL0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
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Pred. No. 3.4e-20;
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/tissue_type="whole body"
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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96.9%;
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Matches 157; Conserva
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JOURNAL
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/issue_type="whole body"
/lab.host="DH10B"
/clone_lib="NHH_ZGC_10"
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
host="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
Bulk tissue was collected from a whole adult_individual
from the Tuebingen strain. list strand cDNA was primed with
a Not I - oligo (dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 k fragments. A
Individualized version of this library is also available
(NHH_ZGC_7). Library was constructed by Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT 15225252 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001739 CF347604
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1 (bases 1 to 787)

1 With-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14695 row: g column: 08
High quality sequence start: 26
High quality sequence stop: 468.
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm.Dao? Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Blosystems
CDNA Library Preparation: Open Blosystems
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001697"
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Best Local Similarity 97.5%;
Matches 153; Conservative
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AQ991732
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AQ991732/c
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KEYWORDS
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AGRNCOURT 15225501 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001611
S', mRNA sequence.
CF347718
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Actimopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Oyprinidae; Danio.
1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela (1939)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAo7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Preparation: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LiAM14655 row: c column: 18
High quality sequence stop: 184.
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                                                                                                                                                                                                                                                                                                                                                                              92.3%; Score 149.6; DB 1497.4%; Pred. No. 1.7e-19; iive 0; Mismatches 4;
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                              High quality sequence stop: (
Location/Qualifiers
http://image.llnl.gov
Plate: LLAM14695 row: i
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Danio rerio
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Best Local Similarity 97.45
Matches 152; Conservative
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                                                                  SOUTHOR
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ORGANISM
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JOURNAL
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CF347718
LOCUS
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KEYWORDS
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/und_type="mRNA"

/db_xref="taxon:7955"

/db_xref="taxon:7955"

/dlab_most="mRNA"

/lab_host="whole body"

/lab_host="while Body"

/lab_host="while Body"

/clone lib="WHI ZGC_10"

/clone lib="WHI ZGC_10"

/note="Vector: pExpressl; Site_1: NotI; Site_2: BcoRV;

Bulk tissue was collected from a whole adult_individual

from the Tuebingen strain. 1st strand cDNA was primed

a Not I - oligo (dT) primer, double-stranded cDNA was

cloned into the Not I and EcoRV sites of pExpress-1.

Library was size-selected for >1 kb fragments. A

normalized version of this library is also available

(NHH ZGC 7). Library was constructed by Open Blosystems

(Huntsville, AL)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ991732 14-AUG-2000 Rfc00380F Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG00380F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 CAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTATATTATATTA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTATTGTATTTATATCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 TACAGGICACIAAIACCAICIAAGIAGIIGGIICAIAGIGACIGCAIAIGIIGIGITIIA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli Klz genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACAGGICACTAATACCAICTAAGTAGTIGATICATAGTGACTGCATATGTTGTGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 149; DB 14; Length 7
Pred. No. 2.2e-19;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 TITIACGTTTCTCGTTCGACTTTTTTGTACAAACTTG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIACGITICACCITCIACTIAINACTACTIG 162
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Department of Balology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae, Photorhabdus.
1 (bases 1 to 756)
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organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Photorhabdus luminescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%;
milarity 96.8%;
Conservative 0,
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Matches 152; Conserv
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98

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Eukaryotta, Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidaa; Rhabditidae; Peloderinae; Caenorhabditis.
(bases 1 to 583)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB403882 583 bp mRNA linear EST 15-MAY-2003
OSTR013H1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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/sex="Hermaphrodite and male"
/rissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmCDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                  66 CAGTATTATGTAGTCTGTTTTTTATGCAAATCTAATTTAATATATTTGATATTTATATCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
              normalized version of this library is also available (NIH ZGC 7). Library was constructed by Open Biosystems (HunEsville, AL)."
                                                                                                                                                                                                                                                                         6 TACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTGTTTTTA
                                                                                                                                                                                                                                                                                                                            39 TACAGGICACTAATACCATCTAAGTACTTGGTTCATAGGGACTGCCTATGTTGTGTTTTA
Library was size-selected for >1 kb fragments. A
                                                                                                                                                                                                                     .
                                                                                                                                                               Length 777;
                                                                                                                                                                                                                  12; Indels
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Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                            85.1%; Score 137.8; DB 14; 92.4%; Pred. No. 3.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TITIACGITICICGITICAGCITITITIATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 ririracdarichicarichachirirgaacaachig 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Caenorhabditis elegans"
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marc Vidal Laboratory
Dana Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB403882.1 GI:30745609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Vidal M
                                                                                                                                                                                         Similarity
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                                                                                                                                                               Query Match
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CB403882/c
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/note="Vector: pExpress1; Site_1: NotI; Site_2: EccRV;
Nute="Vector: pExpress1; Site_1: NotI; Site_2: EccRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EccRV sites of pExpress-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF347686 777 bp mRNA linear EST 18-AUG-2003 AGENCOURT_15225248 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001643
                                                                                                                                                       from strain W14 was size selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                                          509 TrigitianaGGreaceraAracearrraagragragrigarrearagreaceararacerge 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14695 row: e column: 02
High quality sequence start: 373
High quality sequence stop: 674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GITITACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 GITITACANNANTATGTAGTCTGTTTTTTATGCAAATCTAATTTAATATATTGATATT 390
                                                                                                                                                                                                                                                                                                                                                                                  59
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 777)
                                                                                                                                                                                                                                                                                                                                                                         1 TCTGTTACAGGTCA-CTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
           db_xref="taxon:29488"
|clone="PLG00380F"
|dev_stage="pximary phase variant"
|clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                                                                   DB 28; Length 756;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 ATATCATTTAGGTTTCTCGTTCAGCTTTTTTANACTAACTTG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ATATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAACTTG 162
                                                                                                                                                                             kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                Score 140.8; DB 28;
Pred. No. 8.3e-18;
0; Mismatches 9;
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tissue_type="whole body"
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/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                       /note="Genomic DNA
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                                                                                                                                                                                                                                                                86.9%;
93.9%;
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                                                                                                                                                                                                                                                                                                                      153; Conservative
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Best Local Similarity
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CF347686
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Best Local Similarity
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            63
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                                                                                                                                                                     RESULT 13
CB403984/c
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1 (bases 1 to 395)
1 (bases 1 to 395)
2 (Bach-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the encompathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence 20378633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminescens genomic clone PLG02205, genomic survey
                                                                                                                                                                         81 TITTACAGTATTATGTAGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGTTTA
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                                                                                                                    141 TCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGTG
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/clone lib="Photorhabdus luminescens strain W14 M13
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Rfc02205 Photorhabdus luminescens strain W14 M13 library
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            DB 14; Length 583;
                                               Indels
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0; Mismatches 13
          Score 134.6; DB 14
Pred. No. 1.4e-16;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621 Fax: (44) 1225 826779 Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="W14"
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/clone="PLG02205"
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AQ991303.1 GI:9649897
            83.1%;
97.2%;
Query Match
Best Local Similarity 97.25
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Reboul, J. Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Endress, G.M., Li, S., Tarasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Chancette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans Orrecome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                              EST 15-MAY-2003
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/tissue_type="whole animal"
/fdev_tagge="mixed stage"
/clone_lib="AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
286 TTACAGTATTATGTAGTCTGTTTTTTATGCAANATNTNATTTAATATATTGATATTTATA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
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STR015E7_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 1.3e-15; Tindels
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Fax: 617 632 5180
                                                                                                                                     226 TCATTINACGITICINGITCAGNITITITIATACTAAGITG 187
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/mol_type="mRNA"
/strain="N2"
                                                                         123 TCATTTTACGTTTCTCGTTCAGCTTTTTATACTAACTTG
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95.0%;
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Rfc01715 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01715, genomic survey
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A genomic sample sequence of the entomopathogenic bacterium
Aptorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AV, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826721
Fax: (44) 1225 random reads from the M13 library. For This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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1 (Dases 1 to 769)

Effrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
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Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
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/strain="W14"
/strain="W14"
/b_xref="taxon:29488"
/clone="PLG01245"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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Class: shotgun.
Location/Qualifiers
TATCATTTACGTTTCTCGTT 141
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Photorhabdus luminescens
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AQ990470.1 GI:9649064
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AQ990878/c
LOCUS
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AQ990470/c
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GSS 14-AUG-2000

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AQ990878

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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. Agenomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.
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/clone_lib="Photorhabdus luminescens strain W14 M13
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    764
/organism="Photorhabdus luminescens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: ffrench-Constant RH
Department of Balology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 845621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:29488"
/clone="PLG01715"
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GI:9649472
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RESULT 1
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Sequence 175, App
                                                                              9, 2004, 19:34:38; Search time 204.654 Seconds (without alignments) 3982.858 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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Sequence 16, Application US/10310695
Sequence 16, Application US/10310695
Sequence 16, Application US/20040110293A1
GENERAL INFORMATION:
APPLICANT: DROGG, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
APPLICANT: ENENGE, PETER
TITLE OF INVERTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
CURRENT APPLICATION NUMBER: US/10/310, 695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTMARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITIACAGTATIAIGING TOTITITIAIGCAAAATCIAATITIAATATATATATTIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 162; DB 17; Length 162; 100.0%; Pred. No. 1.3e-25;
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                              LENGTH: 162
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Best Local Si
Matches 162;
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 16
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US-10-310-695-14
; Sequence 14, Application US/10310695
; Publication No. US20040110293A1
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; APPLICANT: BENEREL, BARBARA
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEBE:019US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITATGCAAAATCTAATTTAATATTGATATTTA 120
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                                                                                                                                            Sequence 173, Application US/10403232
Publication No. US20030226164A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sutie, Janet Louise
APPLICANT: Chilton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: de Framond, Anic
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 70005USPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.0%; Score 160.4; DB 13; Length 243; Best Local Similarity 99.4%; Pred. No. 3.3e-25; Matches 161; Conservative 0; Mismatches 1; Indels 0;
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       126 TATCATTITACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 167
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Pred. No. 3.3e-25;
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SEQ TWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 243
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CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 14
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US-10-403-232-173
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Best Local Similarity
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US-10-627-711-10

i Sequence 10, Application US/10627711

publication No. US20040115812A1

GENERAL INFORMATION:

APPLICANT: YANG, Shuwei

TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND

TITLE OF INVENTION: SCREENING OF CDNA CLONES

FILE REFERENCE: 51236US

CURRENT APPLICATION NUMBER: US/10/627,711

PRIOR APPLICATION NUMBER: 60/398,589

PRIOR APPLICATION NUMBER: 60/398,589

PRIOR APPLICATION NUMBER: 2002-07-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTING DATE: 2002-07-26

SSO ID NO 10

LENGTH: 168
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                      Sequence 175, Application US/10403232
Publication No. US20030226164A1
GENERAL INFORMATION:
APPLICANT: Suttis, Janet Louise
APPLICANT: Chilton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Rramond, Anic
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 70005USPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 162; DB 13;
; Pred. No. 1.4e-25;
0; Mismatches 0;
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100.0%; Score 162; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-10-403-232-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 162; Conservative
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US-10-403-232-175
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OTHER INFORMATION: attp
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ORGANISM: Eukaryote
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  ; US-10-161-403-72
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                                                                                                                                                            Sequence 8, Application US/10627711
Publication No. US20040115812A1
GENERAL INFORMATION:
APPLICANT: YANG, SHUWE!
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND TITLE OF INVENTION: SCREENING OF CDNA CLONES
TITLE OF INVENTION: SCREENING OF CDNA CLONES
TITLE OF INVENTION SCREENING OF CDNA CLONES
TITLE OF INVENTION NUMBER: US/10/627,711
CURRENT APPLICATION NUMBER: US/10/627,711
PRIOR APPLICATION NUMBER: 2003-07-28
SEACH RILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 248
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99.0%; Score 160.4; DB 17; Length 248;
Best Local Similarity 99.4%; Pred. No. 3.3e-25;
Matches 161; Conservative 0; Mismatches 1; Indels 0;
                                   121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAAGTTG 162
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  121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 162
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APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Fleming, Elena
APPLICANT: Shellard, Joan
ITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE PEFERBNCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT PILING DATE: 2002-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILIATIONION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 282
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Publication No. US20030119104A1
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial
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US-10-627-711-8
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; Sequence 57, Application US/09244805
; Publication No. US20030203840A1
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Geetz, Bernard
; APPLICANT: Geetz, Bernard
; APPLICANT: Scheek, Sigrid
; APPLICANT: Scheek, Sigrid
; APPLICANT: Scheek, Sigrid
; APPLICANT: Scheek, Sigrid
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; APPLICANT: Scheek, Sigrid
; APPLICANT: Scheek, Sigrid
; APPLICANT: ON THEREFOR
; TILLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: 60/074,518
; EARLIER FILING DATE: 1998-02-16
; SCHUMBER OF SEQ ID NOS: 62
; SOFTWARER PERSEQ for Windows Version 4.0
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Length 282;
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Score 160.4; DB 15;
                             Pred. No. 3.5e-25;
0; Mismatches 1
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OTHER INFORMATION: y = C or T

COTHER INFORMATION: n = A,T,C or G

US-09-244-805-57
   99.0%;
   Query Match
Best Local Similarity 99.4
Matches 161; Conservative
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4130 TTTTÄCAGTATTÄTGTGTÄGTCTGTTTTTTÄTGCAAAATCTÄÄTTTAATATATTGATATTTA 4189
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                                                                                                                                                                                                                          Query Match
99.0%; Score 160.4; DB 17; Length
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels
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                                                       NAME/KEY: misc feature
| LOCATION: (1)...(1763)
| OTHER INFORMATION: y = C or T
| COTHER INFORMATION: n = A,T,C or G
US-10-792-481-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Fleung, Josephine
APPLICANT: Fleung, Josephine
APPLICANT: Stewart, Sandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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        ORGANISM: Eukaryote FEATURE:
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LENGTH: 4346
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                                                                           APPLICANT: Worley, Paul F.
APPLICANT: Worley, Paul F.
APPLICANT: Lanahan, Anthony
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE REPERENCE: JHUJ530-3
FILE REPERENCE: JHUJ530-3
CURRENT APPLICATION NUMBER: 00/074,518
PRIOR PILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/074,135
PRIOR APPLICATION NUMBER: 60/074,135
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-02-06
SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 160.4; DB 11; Length 1763; Pred. No. 5.9e-25; 0; Mismatches 1; Indels 0;
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| APPLICANT: Worley, Paul F. |
| APPLICANT: Lanahan, Anthony |
| APPLICANT: Lanahan, Anthony |
| APPLICANT: Goetz, Bernard |
| APPLICANT: Goetz, Bernard |
| APPLICANT: Goetz, Heimisch, Holger |
| APPLICANT: Scheek, Sigrid |
| APPLICANT: Scheek, Sigrid |
| APPLICANT: Nikolich, Karoly |
| APPLICANT: Nikolich, Karoly |
| APPLICANT: Nikolich, Raroly |
| APPLICANT: Nikolich, Raroly |
| APPLICANT: Nikolich, Raroly |
| TITLE OF INVENITON: IMMEDIATE EARLY GENES AND METHODS OF USE |
| TITLE OF INVENITON: THEREFOR |
| TITLE OF INVENITON: THEREFOR |
| FILE REFERENCE: 10496/004001 |
| CURRENT APPLICATION NUMBER: US/09/244,805 |
| PRIOR FILING DATE: 1999-02-05 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-06 |
| SOFTWARRE FASTERQ for Windows Version 4.0 |
| SEQ ID NO 57 |
| LENGTH: 1763
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Sequence 57, Application US/09245277 Publication No. US20030211984A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/10792481 Publication No. US20040152658A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1) ... (1763)
OTHER INFORMATION: \gamma = C or T
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.4%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Eukaryote
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US-10-792-481-57/c
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Sequence 24, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE DE INVENTION: Using recombinational cloning
                                                                                                                                                                                                                                                                                                      APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
ITILE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16578 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 16637
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Pred. No. 5.8e-23;
0; Mismatches 6; Indels
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CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26
                                                121 TATCATTTTACGTTTCTCGTTCAGCTT
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; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 96.3%;
Matches 156; Conservative
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Best Local Similarity 96.3%;
Matches 156; Conservative
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LENGTH: 17458
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US-10-055-001A-24
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Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Waing recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
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                                                                                                                                        APPLICANT: DROGE, PETER
APPLICANT: ENENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 2
LENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: acceptor vector phellsGatell US-10-055-001A-25
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                                                             Sequence 2, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Matches 158; Conservative
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LENGTH: 17458
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1 totgttacaggtcactaata......agctttttatactaacttg 162
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Describtion	Sequence	Segue	cteriop	Segue	Immediat	M17028 P.falciparu	AF178449 Integrati	AFI/8450 Integrati AF271663 Cloning v	U13848 pExcell clo	AF178452 Integrati	Integrat	AXII3/40 Sequence	AX113746 Sequence	U66308 Expression	AK399301 Sequence	AX113747 Sequence	AF178451 Integrati	loning	U39285 Cloning vec	loning	J02459 Bacteriopha	BD263378 Compositi	BD263379 Compositi	BD263377 Compositi	BD263381 Compositi	AJ311874 Cloning v	AJ311874 Cloning v RD263225 Compositi	AX787499 Sequence	Composit	Composit	Composit	BD263381 Compositi	Composit	Composit.	DIAGSAZA COMPOSICA	8.1	DNA linear PAT 21-MAR-2001	
SUMMARIES	AX092115	AX092	LAMINTA	MACHSS	BD225	PFAHRPC	AF17844	AF2716	XXU1384	AF17845	AF17845	AX11374	AX11374	U66308	AK39930		AF17845	CVU39	CVU3928	CVU3769	LAMCG	BD26337	BD26337	BD26337		CVE311	CVE31187	AX78749	BD26338	BD26337	BD26337	BD26338	BD26338	BD26340	200	ALIGNMENTS	162 bp nt WO0116345.	358
Length DB	162 6			010	763	758	485	100	190	549	549	100	826	000	043	071	7176	529	2531		8502	204	208	470	7 00 U	8691	691		165	204	470		156	584			from Patent	GI:1344435
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Result No. Score	1 162	160	160	5 160	160	8 160	160	160	2 160	13 160	160	160	17 160	18 160	160	21 160	2 160	3 160	160	9 160	7 160.	150.	30 150.	150.	33 150.	34 150.	150.	7 150.	38 149.	149.	149.	2 149.	43 149.	4 149.	*		RESULT 1 AX092115 LOCUS DEFINITION SE	

		162 bp DNA linear PAT 21-MAR-200;	00116345.						Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,	richia.			Sequence-specific dna recombination in eukaryotic cells	3-MAR-2001;	
		AX092115	Sequence 4 from Patent W00116345	AX092115	AX092115.1 GI:13444358	•	Escherichia coli	Escherichia coli	Bacteria; Proteobacteria;	Enterobacteriaceae; Escherichia.	·	Droege, P.	Sequence-specific dna rec	Patent: WO 0116345-A 4 08-MAR-2001;	
KENOLT I	AX092115	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	

FEATURES

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ILAMINTATT

Bacteriophage lambda int gene region.

M23841

M23841

M23841. GI:215177

Site-specific recombination.

Bacteriophage lambda

TSM Bacteriophage lambda

Viruses; dsDNA viruses.

CE Lambda-like viruses.

CE Lambda-like viruses.

CE Candovirales; Siphoviridae;

Lambda-like viruses.

CE Removal of a terminator structure by RNA processing regulates int

gene expression.
PAT 21-MAR-2001
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                                                                                                      Bacteriophage lambda
Bacteriophage lambda
Viruses; dSDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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                                                                                                                                                                                                                              Sequence-specific dna recombination in eukaryotic cells Patent: WO 0116345-A 2 08-MAR-2001; Droege, Peter (DE) Location/Qualifiers
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  linear
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Location/Qualifiers
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Pred. No. 1.2e-20;
0; Mismatches 1;
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Pred. No. 1.3e-20;
0; Mismatches 1;
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    DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:10710"
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/mol_type="genomic_DNA"
/db_xref="taxon:10710"
AX092113 243 bp
Sequence 2 from Patent WO0116345.
AX092113
                                                               AX092113.1 GI:13444356
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Best Local Similarity 99.4%;
Matches 161; Conservative (
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Best Local Similarity 99.4'
Matches 161; Conservative
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84242838
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Bacteriophage lambda site specific recombinant DNA (attR).
M12459
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Viruses, dsDNA viruses, no RNA stage, Caudovirales, Siphoviridae,
Lambda-like viruses.
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                                                                                                                                                                          Length 162;
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Bushman,W., Thompson,J.P., Vargas,L. and Landy,A.

Control of directionality in lambda site specific science 230 (4728), 906-911 (1985)
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100.0%; Score 162; DB 7;
Best Local Similarity 100.0%; Pred. No. 7.1e-21;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                     100.0%; Score 162; DB 6;
100.0%; Pred. No. 7.2e-21;
ive 0; Mismatches 0;
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/mol type="genomic DNA"
/db xref="taxon:10710"
                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:562"
                                                               organism="Escherichia"
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Location/Qualifiers
                          Location/Qualifiers
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    Peter (DE)
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Best Local Similarity 100.
Matches 162; Conservative
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      Droege,
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Rattus norvegicus
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PC C12N15/00,C12N5/00
CC n is either a t
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                                                                                                                                        sex="male"
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  Fax:+81-426-76-4517)
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Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Bharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518,
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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TITIACAGTATTATGTAGTCTGTTTTTTTTGCCAAAATCTAATTTAATATATTGATATTTA 140
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hydroxysteroid sulfotransferase subunit.
hydroxysteroid sulfotransferase subunit.
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 1668)
Ogura, K., Satsukawa, M., Kato, K., Okuda, H. and Watabe, T.
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
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Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
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.larity 99.4%; Pred. No. 1.1e-20;
Conservative 0; Mismatches 1; Indels 0
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                                                                               139 TATCATTTTACGTTTCTCAGTTTTTTTATACTAAGTTG
                                                             121 TATCATTTTACGTTTCTCGTTCAGCTTTTTATACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Nicotiana tabacum"
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Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
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/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                               Nicotiana tabacum (common tobacco)
                                                                                                                                                                                         Sequence 1 from Patent W00121780.
AX101000
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2 (bases 1 to 1668)
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Matches 161; Conserv
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QLFPKSFFSSKAKVIYIMRNPRÖVFVSGYFFWNSVKFVKKPKSWQQYFEWFCQGNVIY
GSWYDHIHGWMPMRBKKNFLLLSYEBLKQDTRRTVBKTCQFLGKTLEPBELNLILKNS
SPGSKKENKMSNFSLLSVDFVBEKAQLLRKGISGDWKNHLTVAQAEAFDKLFQEKMTD
LPRELEPWE"
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SGTNWLIEILCLIHSNGDFKWIQSVPIWERSPWVBTEMGYKLLSEEEGFRLFSSHLPI
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CI2N15/09,A61K31/711,A61K48/00,A61P25/00,A61P25/28,C07H21/04, PC
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PN 02-002512772-A/49
PD 08-MAY-2920
PP 05-FEB-1999 UP 2000530634
PR 09-FEB-1999 US 60/074135,12-FEB-1999 US 60/074518
PAULE WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                            /organism="Macaca fascicularis"
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611. .1468
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Location/Qualifiers
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translation="MVLVTCNRALAQGDFCLLALIFCHQTCRTPEKHKASQSSAKLVS
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Integration vector pCD11PKS chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
AF178449
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Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
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/note="putative VBCTOR sequence Bacteriophage lambda
(J02459); putative"
2525..2758
/gene="histidine rich protein C"
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
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complement (2596. .>2758)
/gene="histidine rich protein D"
         'gene="histidine rich protein E"
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Pred. No. 7.6e-21;
0; Mismatches 1;
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/gene="histidine rich protein
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Integration vector pCD11PKS
artificial sequences; vectors.
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Matches 161; Conservative
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1 (bases 1 to 2758)
Lenstra,R., Alvodata; Apicomplexa; Haemosporida; Plasmodium.

Lenstra,R., d'Auriol,L., Andrieu,B., Le Bras,J. and Galibert,F.

Cloning and sequencing of Plasmodium falciparum DNA fragments

containing repetitive regions potentially coding for histidine-rich

proteins: identification of two overlapping reading frames

Biochem. Biophys. Res. Commun. 146 (1), 368-377 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source text: P.falciparum, cDNA to mRNA, clone M4
Location/Qualifiers
                                                                                                                                                                                                               ;
0
                                                                                                                                                                          Length 1763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MI7028.1 GI:160339
histidine-rich protein.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                             Indels
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complement (828. .1589)
//gene="histidine rich protein E"
complement (828. .1589)
                                                                                                                                                                        99.0%; Score 160.4; DB 6; 99.4%; Pred. No. 8.4e-21;
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P.falciparum histidine-rich protein genes.
M17028
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/mol type="genomic DNA"
/mb_xref="taxon:5833"
1. .234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="histidine rich protein B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124. .1072
|gene="histidine rich protein B"
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Location/Qualifiers (1). (1763). Focation/Qualifiers
                                                                        /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db xref="taxon:10116"
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/gene="histidine rich
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ACCESSION
VERSION
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                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                              /tränslation="MEKKITGYTTVDISQWHRKEHFEAPGSVAQCTYNQTVQLDITAF
LITYVKKNRKFREYPAFHILLARLMNAHPERMAMANGDELVINDSVHEYTVFHEQTETF
SSIMSEYHDDFRQFLAIYSQDVACYGENLAYFPKGFIEMFFVSANPWVSFTSPDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="MTMITPSAQLTLTKGNKSWVPGPPSRSTVSISLISNSCSPGDPL
VLERPPPRWSSNSPYSESYYARSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEB
ARTDRPSQQLRSLNGEWLTRPVAAH"
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(18-AUG-1999) Microbiology, Iowa State University, 207 Building, Ames, IA 50011, USA Location/Qualifiers
                                                                                                                                                                                                         /note="attP; attachment site from bacteriophage lambda"
complement(1327. .1986)
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1 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and
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Pred. No. 7.2e-21;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="beta-galactosidase alpha peptide"
'protein id="AAF86670.1"
'db_xref="GI:9294786"
                                                                                                                                                                                                                                                                                                                    /transl_table=11
product="chloramphenicol transacetylase"
protein id="MAF86671.1"
/db_xref="GI:9294787"
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                                                                        /organism="Integration vector pCD11PKS"
mol_type="genomic DNA"
db_xref="taxon:106602"
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/note="multiple cloning site"
                                                                                                                            lab hst="Escherichia coli"
. .385
note="R6Kgamma"
                                                                                                                                                                                                                                                                   complement (1327. .1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="lacza"
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Best Local Similarity 99.4%;
Matches 161; Conservative (
                                                                                                                                                                                                                                                                                   gene="cat"
                                                                                                                                                                                                                                                  /gene="cat
                                                                                                                                                                                         668. .915
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/product="beta-galactosidase alpha peptide"
/protein id="AAF86672.1"
/brotein id="AAF86672.1"
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/brotein id="AAF86672.1"
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/translation="WIMPIFSAGITLITKGNKSWSSTAVAAALBLVDPPGCRNSISSLS
IPSTSRGGPVPNSPYSESYYARSLAVULQRRDWENPGVTQLNRLAAHPPFASWRNSBE
ARTDRPSQQLRSLNGEWLTRPVAAH"
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                                                                                       2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Submission
Submitted (la8-440-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                /note="attP; attachment site from bacteriophage lambda"
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lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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Pred. No. 7.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4105 bp DNA complete sequence.
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/note="multiple cloning site"
                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db xref="taxon:106603"
/lab host="Escherichia coli"
1. 385
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complement (2754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1327.
                                                                                                                                                                                                                                                                                                                                                                   /note="R6Kgamma"
668. .915
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="cat"
/codon_start=1
/transl_table=1
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99.48;
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Matches 161; Conservative
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pExCell cloning vector, complete sequence
                                                                                      unidentified cloning vector unidentified cloning vector
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transl_table=
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/gene="lac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="bla"
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gene="lac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="bla"
                                                                                                                                          1 (bases 1 to 4190)
Malone, J.A.
                                                                                                                                                                                                                                  (bases 1 to 4190)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="lac"
                                 GI:595702
                                                                                                                                                                                                                                               Malone, J.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                          ...4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4. .894
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                  U13848
U13848.1
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 DEFINITION
                                                                                                          ORGANISM
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JOURNAL
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                  ACCESSION
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KEYWORDS
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                                                                                                                                                                              TITLE
                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AaF82364.1"
/db_xref="G1:902233"
/translation="MIPRDPRSPAPDLSAINQPAGRAERRSGPATLSASIQSINCCRE
ARVSSSPVNSLRNVYAIATGIVVSRSSFGMASFSSGSQRSRRVT"
                                                                                                                                                                                                                                                                                                                                                                                                 GKPDAPELFLKHGKGSVANDVTDEMVRLNWLTEFMPLPTIKHFIRTPDDAWLLTTAIP
                                                                                                                                                                                                                                                                                                                                                                                                              GKTAFQVLEEYPDSGENIVDALAVFLRRLHSIPVCNCPFNSDRVFRLAQAQSRMNNGL
VDASDFDDERNGWPVEQVWKEMHKLLPFSPDSVVTHGDFSLDNLJFDEGKLIGCIDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IELDLNSGKILLESFRPEERFPMMSTFKVLLCGAVLSRVDAGGEGLGRRIHYSQNDLVB
SYVTEKHLIDGMYVRELCSAAITMSDNTAANLLTTIGGGFEETAFLHMGDHYTRL
DRWEPELNEAL BYDDEDTTMPWAATTLIKKLLIGELITLASRQEITDMMEDRYKAGPL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATWDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                              translation="MSHIQRETSCSRPRINSNMDADLYGYKWARDNVGQSGATIYRLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
             cloning vector pLDR9
artificial sequences; vectors.

(basel to 4105)
Wiencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and August,P.R.
Direct Submission
Submitted (24-MAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVGIADRYQDLAILWNCLGEFSPSLQKRLFQKYGIDNPDMNKLQFHLMLDEFF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                      product="aminoglycoside 3' phosphotransferase"
protein id="AAF82363.1"
db_xref="GI:9022392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4105;
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                                                                                                                                                                                                                                                   1167 .1031
function="confers kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAICATITITACGITICICGITICAGCITITITATACIAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="hypothetical 9.2 kD protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 160.4; DB 12;
Pred. No. 6.9e-21;
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                                                                                                                                                                                             organism="Cloning vector pLDR9"
mol_type="genomic DNA"
db_xref="taxon:130501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "EC_number="3.5.2.6"
note="derived from pMMB66EH"
codon start=1
frans] table=11
product="beta-lactamase"
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db_xref="GI:9022391"
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trans1 table=
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99.4%;
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/note="attP"
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   Cloning vector pLDR9
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Best Local Similarity
Matches 161; Conserv
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XXU13848/c
LOCUS
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                  ORGANISM
                                                                                                                       JOURNAL
                                                      REFERENCE
                                                                       AUTHORS
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circular SYN 13-DEC-1994

DNA

4190 bp

XXU13848

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DRWEPELNEAI PNDERDTTMPVAMATTILRKLITGELLTLASROOLIDWIEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="plasmid origin of replication; base 1653 represents
the first base of the newly synthesized strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Multiple Cloning Site (MCS); contains unique sites for Sfil, Xhol, EcoRl, BamHI, Notl, Mlul, HindIII" complement (2155. .2174)
/gene="T7 RNA polymerase" complement (2155. .2174)
/gene="T7 RNA polymerase" 2933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (19-AUG-1994) James A. Malone, International Technical
Services, Molecular Biology Reagents Division, Pharmacia Blotech
Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA
Location/Qualifiers
                                                                                                                                                                                        pExCeli: A multifunctional cloning vector that is released from lambda ExCell by in vivo excision Unpublished (1994)
T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/lab_host="Escherichia coli"
34. 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transī table=11
/producE="lacz alpha peptide"
/protein_id="AAA57084.1"
/db_xref="GI:595703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .073. .2089
gene="SP6 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .073. .2089
'gene="SP6 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
transl_table=11
product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAA57085.1"
db_xref="GI:595704"
                                                                                                                    artificial sequences; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="lac operator"
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                                                                                                                                                                                                                                                                                                                                                                    4089 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT 4030
                                                                                                                                                                                                                                                                                                                                                                                                                                           SYN 20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integration vector pCD13PKS aminoglycoside adenyltransferase (aadh) and beta-galactosidase alpha peptide (lacZa) genes, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                 09
/note="bacteriophage fl origin of replication for
production of single-stranded DNA; base 2933 represents
the first base of the newly synthesized single strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 4549)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-R401999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="attP; attachment site from bacteriophage lambda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 4549.)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Bscherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                        61 TITIACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            DB 12; Length 4190;
                                                                                                                                                                                                                                                                                               0;
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|trans1_table=11
|product="aminoglycoside adenyltransferase"
|protein_id="AAF86677.1"
|db_xref="GI:9294796"
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3969 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAAGTTG 3928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Integration vector pCD13PKS"
                                                                                                                                                                                                                                                         Score 160.4; DB 12;
Pred. No. 6.9e-21;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                             /note="attP gene from lambda"
3932. 3947
/gene="attP"
/note="att core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:106605"
/lab_host="Escherichia coli"
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Integration vector pCD13PKS
artificial sequences; vectors.
                                                     direction=right
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                                                                      3847. .4094
/gene="attP"
3847. .4094
/gene="attP"
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                                                                                                                                                                                                                                                     Sectory march
Best Local Similarity 99.4%;
Matches 161; Conservative
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VTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRIASRADQLEBEFVHVVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integration vector pCD13PSK aminoglycoside adenyltransferase (aadA) and beta-galactosidase alpha peptide (lacZa) genes, complete cds. AF178453
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Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Blatt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Submitted (18-40G-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
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/note="attP; attachment site from bacteriophage lambda"
complement(1798. .2652)
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Platt, R., Drescher, C., Park, S. K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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Pred. No. 6.8e-21;
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                                                                                                                     complement (3818. .4201)
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Integration vector pCD13PSK
artificial sequences; vectors.
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/gene="lacZa"
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db_xref="GI:9294799"
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1. .5641
/organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="multiple cloning site"
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Chitobiase as a reporter enzyme
Patent: WO 0127322-A 13 19-APR-2001,
Elitra Pharmaceuticals, Inc. (US)
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WO0127322.
 .2652)
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complement(3818. .4201)
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Sequence 13 from Patent
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Matches 161; Conservative
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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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